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From: Mertz, Prema
Sent: Tuesday, July 05, 2005 2:37 PM
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Subject: 10/750,797

CRF

Please search SEQ ID NO:1-2 with protein databases.

Thanks.

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Searcher: _____
Searcher Phone: 2-_____
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Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
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Other(Specify): _____

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OW protein - protein search, using sw model

Run on: July 9, 2005, 12:41:15 ; Search time 111.181 Seconds

(without alignments)
801.415 Million cell updates/sec

Title: US-10-750-797-1

Perfect score: 896

Sequence: 1 TPLGPASSLPQSLFKLCLEQ.....SHLQSFLEVSRYVRLHQAQ 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of residues predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	896	100.0	200	Q8N4W3	Q8N4W3 homo sapien
2	884.5	98.7	207	CSF3_HUMAN	P09919 homo sapien
3	744	83.0	194	CSF3_FELCA	O02708 felis silve
4	744	83.0	195	O9GJTO	O9GJTO felis silve
5	738	82.4	174	CSF3_SHEEP	O28746 ovib aries
6	734	81.9	175	CSF3_CANFA	P35834 canis famli
7	727	81.1	195	CSF3_BOVIN	P35833 bos taurus
8	702	78.3	195	CSF3_PIG	O02837 sus scrofa
9	641	71.5	208	CSF3_MOUSE	P09920 mus musculi
10	634	70.8	214	P97712	P97712 rattus norv
11	511	57.0	127	Q8MKE0	Q8MKE0 equus cabal
12	304	33.9	201	MGP_CHICK	P13854 gallus gall
13	111	12.4	241	O90Y10	O90Y10 gallus gall
14	110.5	12.3	212	O8M775	O8M775 sus scrofa
15	108	12.1	208	O9XT80	O9XT80 delphinape
16	106.5	11.9	212	IL6_PYG	P26893 sus scrofa
17	101	11.3	205	IL6_ORCOR	Q28747 orcinus orc
18	100	11.2	208	IL6_HORSE	Q95181 equus cabal
19	96	10.7	189	O6N282	O6N282 homo sapien
20	96	10.7	189	O6N2A5	O6N2A5 homo sapien
21	95	10.6	208	IL6_FELCA	P41683 felis silve
22	94.5	10.5	455	O8D706	O8D706 vibrio vuln
23	94	10.5	345	O9PCT16	O9PCT16 vibrio chol
24	93	10.4	189	O9NPF7	O9NPF7 homo sapien
25	91	10.2	189	O6N280	O6N280 homo sapien
26	89.5	10.0	214	O8MKE5	O8MKE5 sus scrofa
27	89.5	10.0	2175	HMCTU_DROME	P10180 drosophila
28	88.5	9.9	666	O9A523	O9A523 calobacter
29	88.5	9.9	786	O91019	O91019 pseudomonas
30	88.5	9.9	1931	O8BJY3	O8BJY3 stigmatella
31	86	9.6	208	IL6_BOVIN	P26892 bos taurus

32	86	9.6	502	2	Q34008	Q34008 beta vulgar
33	86	9.6	788	2	O8CF87	O8CF87 mus musculi
34	86	9.6	850	2	O7TQ21	O7TQ21 mus musculi
35	86	9.6	851	2	O8CF88	O8CF88 mus musculi
36	86	9.6	852	2	O81179	O81179 mus musculi
37	85.5	9.5	211	2	O865W7	O865W7 camelus bac
38	85.5	9.5	1288	2	O8LQK8	O8LQK8 oryza sativ
39	85	9.5	193	2	O9N2H9	O9N2H9 sus scrofa
40	85	9.5	208	2	O6V919	O6V919 bubalus bub
41	84.5	9.4	209	1	IL6_PHOVI	O28819 phoca vitul
42	84.5	9.4	211	1	IL6_LAMGL	O85X6 lama glama
43	84.5	9.4	455	2	O7MDW7	O7MDW7 vibrio vuln
44	84	9.4	175	2	O9TTH4	O9TTH4 actus nigri
45	84	9.4	208	1	IL6_CAPHI	O28319 capra hircu

ALIGNMENTS

RESULT 1

ID	Q8N4W3	PRELIMINARY:	PRT:	200 AA.
AC	Q8N4W3			
DT	01-OCT-2002 (TrEMBLrel. 22, Created)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DE	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	Colony stimulating factor 3, isoform C.			
GN	Name=CSF3;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxId=9606;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Skin;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diachenko L., Marueta K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Villalón D.K., Wuzny K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,			
RA	Fahy J., Helton E., Keltman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley A.C., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Krzywniak M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,			
RA	Jones S.J., Mair M.A.,			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Skin;			
RA	Straussberg R.L.,			
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: BC033245; AAH3245.1;			
DR	HSSP: P09819; IGNC.			
DR	GO: GO:0005576; C:extracellular; IEA.			
DR	GO: GO:0005125; F:cytokine activity; IEA.			
DR	GO: GO:0005138; F:interleukin-6 receptor binding; IEA.			
DR	GO: GO:0006955; P:immune response; IEA.			
DR	InterPro: IPR009079; 4 helix cytokine.			
DR	InterPro: IPR003629; GCSF_MGF.			
DR	InterPro: IPR003573; IL6_MGF_GCSF.			
DR	InterPro: IPR003574; Interleukin_6.			
DR	Pfam: PF00489; IL6_1.			
DR	PRINTS: PR00433; IL6GCSFMGF.			

DR PRINTS: PR00434; INTERLEUKIN6.
 DR Prodom: PD008388; GCSF MGF: 1.
 DR Prodom: PD004356; Interleukin_6; 1.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR SEQUENCE 200 AA; 21543 MW; 8648AA55B329A96C CRC64;
 Query Match 100.0%; Score 896; DB 2; Length 200;
 Best Local Similarity 100.0%; Pred. No. 5.2e-74;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPLGSPASLPSFLKCKEYVRKIQDGAALOEKLCATYKCHPELVYLGHSLGIPWAP 60
 DB 27 TPLGSPASLPSFLKCKEYVRKIQDGAALOEKLCATYKCHPELVYLGHSLGIPWAP 86
 QY 61 LSSCPQALQAGCISQHSGLFLYQGLQALGISELPGLDTLQLDVADFATTIQQ 120
 DB 87 LSSCPQALQAGCISQHSGLFLYQGLQALGISELPGLDTLQLDVADFATTIQQ 146
 QY 121 MEELGMALOPTQGAMPAPASAFORRAGVTVASHLOSFLSVSYRVLRHLAQP 174
 DB 147 MEELGMALOPTQGAMPAPASAFORRAGVTVASHLOSFLSVSYRVLRHLAQP 200
 RESULT 2
 CSF3 HUMAN STANDARD; PRT; 207 AA.
 ID CSF3_HUMAN P09919;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Granulocyte colony-stimulating factor precursor (G-CSF) (Pluripoietin)
 DE (Flgrastim) (Lenograstim).
 OS Homo sapiens (Human).
 GN Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=66118679; PubMed=3484805;
 RA Nagata S., Tsuchiya M., Asano S., Kaziro Y., Yamazaki T., Yamamoto O.,
 RA Hirata Y., Kubota N., Oheda M., Nomura H., Ono M.;
 RT "Molecular cloning and expression of cDNA for human granulocyte
 RT colony-stimulating factor.";
 RL Nature 319:415-418 (1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=66220137; PubMed=2423327;
 RA Nagata S., Tsuchiya M., Asano S., Yamamoto O., Hirata Y., Kubota N.,
 RA Oheda M., Nomura H., Yamazaki T.;
 RT "The chromosomal gene structure and two mRNAs for human granulocyte
 RT colony-stimulating factor.";
 RL EMBO J. 5:575-581 (1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87196936; PubMed=3494801;
 RA Devlin J.C., Devlin P.E., Myambo K., Lilly M.B., Rado T.A.,
 RA Warren M.K.;
 RT "Expression of granulocyte colony-stimulating factor by human cell
 RT lines.";
 RL J. Leukoc. Biol. 41:302-306 (1987).
 RN [4]
 RP SEQUENCE FROM N.A. AND VARIANTS MET-157 AND THR-174.
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RT "Seattlesp. NHBI HL6682 program for genomic applications, UW-
 RT FHRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
 RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 19-207 FROM N.A.
 RX MEDLINE=66151684; PubMed=2420009;
 RA Souza L.M., Boone T.C., Gabrilove J., Lai P.H., Zeebo K.M.,

RA Murdock D.C., Chazin V.R., Bruszewski J., Lu H., Chen K.K.,
 RA Barendt J., Platzer B., Moore M.A.S., Mettelmann R., Welte K.;
 RT "Recombinant human granulocyte colony-stimulating factor: effects on
 RT normal and leukemic myeloid cells.";
 RL Science 232:61-66 (1986).
 RN [6]
 RP CARBOHYDRATE-LINKAGE SITE.
 RX MEDLINE=93293942; PubMed=7685769;
 RA Clogston C.L., Hu S., Boone T.C., Lu H.S.;
 RT "Glycosidase digestion, electrophoresis and chromatographic analysis
 RT of recombinant human granulocyte colony-stimulating factor glycoforms
 RT produced in Chinese hamster ovary cells.";
 RL J. Chromatogr. A 637:55-62 (1993).
 RN [7]
 RP STRUCTURE BY NMR.
 RX MEDLINE=93106200; PubMed=1281794; DOI=10.1016/0014-5793(92)81521-W;
 RA Zink T., Rose A., Ambrosius D., Rudolph R., Holak T.A.;
 RT "Secondary structure of human granulocyte colony-stimulating factor
 RT derived from NMR spectroscopy.";
 RL FEBS Lett. 314:435-439 (1992).
 RN [8]
 RP STRUCTURE BY NMR.
 RX MEDLINE=94304859; PubMed=7518249;
 RA Zink T., Rose A., Luers K., Gieslar C., Rudolph R., Holak T.A.;
 RT "Structure and dynamics of the human granulocyte colony-stimulating
 RT factor determined by NMR spectroscopy. Loop mobility in a four-helix-
 RT bundle protein.";
 RL Biochemistry 33:8453-8463 (1994).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=93281718; PubMed=7685117;
 RA Hill C.P., Ostlund T.D., Eisenberg D.;
 RT "The structure of granulocyte-colony-stimulating factor and its
 RT relationship to other growth factors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:5167-5171 (1993).
 CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
 CC cytokines that act in hematopoiesis by controlling the production,
 CC differentiation, and function of 2 related white cell populations
 CC of the blood, the granulocytes and the monocytes/macrophages. This
 CC CSF induces granulocytes.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=long;
 CC IsoId=P09919-1; Sequence=Displayed;
 CC Name=short;
 CC IsoId=P09919-2; Sequence=VSP_002673;
 CC -1- PTM: O-glycan consists of Gal-GalNAc disaccharide which can be
 CC modified with up to two sialic acid residues (done in
 CC recombinantly expressed G-CSF from CHO cells).
 CC -1- PHARMACEUTICAL: Available under the names Neupogen or Granulokine
 CC (Amgen/Roche) and Granocyte (Rhône-Poulenc). Used to treat
 CC neutropenia (a disorder characterized by an extremely low number
 CC of neutrophils in blood).
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
 CC -1- CAUTION: Ref.4 misquotes the gene name as "CSF1".
 CC -1- DATABASE: NAME=Neupogen/Granulokine;
 CC NOTE=Clinical information on Neupogen/Granulokine;
 CC WWW=<http://www.neupogen.com/>.
 CC -----
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 CC -----
 DR EMBL: X03438; CAA27168.1; -;
 DR EMBL: M13008; AAA03056.1; -;
 DR EMBL: X03656; CAA27291.1; -;
 DR EMBL: X03655; CAA27290.1; -;

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DR EMBL; AF388025; AAK62469.1; -.
DR EMBL; M17706; AAA5882.1; -.
DR PIR; A24573; A24573.
DR PIR; A25093; FOHUGL.
DR PDB; 1CD9; X-ray; A/C=30-207.
DR PDB; 1GNC; NMR; @=30-207.
DR PDB; 1PGR; X-ray; A/C/E/G=30-207.
DR PDB; 1RKG; X-ray; A/B/C=31-207.
DR GeneW; HGNC:2438; CSF3.
DR MIM; 138970; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005130; F:granulocyte colony-stimulating factor recep. .; TAS.
DR GO; GO:0007275; P:development; TAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR 3D-structure; Alternative splicing; Cytokine; Glycoprotein;
KW Growth factor; Pharmaceutical; Polymorphism; Signal.
KV
FT SIGNAL 1 30
FT CHAIN 31 207
FT DISULFID 69 75
FT DISULFID 97 107
FT CARBOHYD 166 166
FT VASPLIC 66 68
FT VARIANT 157 157
FT VARIANT 174 174
FT HELIX 41 65
FT HELIX 69 71
FT HELIX 77 86
FT TURN 87 88
FT HELIX 105 124
FT TURN 125 127
FT TURN 130 132
FT HELIX 133 156
FT TURN 157 158
FT HELIX 176 203
FT TURN 204 204
SQ SEQUENCE 207 AA; 22293 MW; 421F635ECC776996 CRC64;

Query Match 98.7%; Score 884.5; DB 1; Length 207;
Best Local Similarity 98.3%; Pred. No. 6.1e-73;
Matches 174; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 TPLGASSTLPSFLKLCLEQVRKIQGDGAALQEK---CATYKLCHEPELVILGSHGIP 57
DB 31 TPLGASSTLPSFLKLCLEQVRKIQGDGAALQEKVSECATYKLCHEPELVILGSHGIP 90
QY 58 WAPLSSCSQALQAGCISQLSHGLFLYQGLQALLEGISPELGPITDLOLVADPATTI 117
DB 91 WAPLSSCSQALQAGCISQLSHGLFLYQGLQALLEGISPELGPITDLOLVADPATTI 150
QY 118 WQNEBELGMAPALOPTGAMPAPAFAPORRAGGVIVASHLQSFLEVSRYVLRHLAQP 174
DB 151 WQNEBELGMAPALOPTGAMPAPAFAPORRAGGVIVASHLQSFLEVSRYVLRHLAQP 207

RESULT 3
CSF3_FELCA STANDARD; PRT; 194 AA.
AC 002708;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Granulocyte colony-stimulating factor precursor (G-CSF) (Fragment).

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GN Name=CSF3;
OS Fells silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_Taxid=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=European Shorthair; TISSUE=Lung;
RX MEDLINE=21389237; PubMed=11497496; DOI=10.1006/cyto.2001.0910;
RA Dunham S.P., Onions D.E.;
RT Isolation, nucleotide sequence and expression of a cDNA encoding
RT feline granulocyte colony-stimulating factor.";
RL Cytokine 14:347-351(2001).
CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC cytokines that act in hematopoiesis by controlling the production,
CC differentiation, and function of 2 related white cell populations
CC of the blood, the granulocytes and the monocytes-macrophages. This
CC CSF induces granulocytes (By similarity).
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: O-glycosylated (By similarity).
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; Y08558; CAA69853.1; -.
DR PIR; T09255; T09255.
DR HSSP; P09919; 1RKG.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR CYTOKINE; Glycoprotein; Growth factor; Signal.
FT NON_TER 1 1
FT SIGNAL <1 20
FT CHAIN 21 194
FT DISULFID 56 62
FT DISULFID 84 94
FT CARBOHYD 153 153
SQ SEQUENCE 194 AA; 21154 MW; F72B7AB3DAE7385E CRC64;

Query Match 83.0%; Score 744; DB 1; Length 194;
Best Local Similarity 81.0%; Pred. No. 4.2e-60;
Matches 141; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 1 TPLGASSTLPSFLKLCLEQVRKIQGDGAALQEK---CATYKLCHEPELVILGSHGIP 60
DB 21 TPLGASSTLPSFLKLCLEQVRKIQGDGAALQEKCAHKKCHEPELVILGSHGIP 80
QY 61 LSSCPSQALQAGCISQLSHGLFLYQGLQALLEGISPELGPITDLOLVADPATTIWQ 120
DB 81 LSSCPSQALQAGCISQLSHGLFLYQGLQALLEGISPELGPITDLOLVADPATTIWQ 140
QY 121 MEELGMAPALOPTGAMPAPAFAPORRAGGVIVASHLQSFLEVSRYVLRHLAQP 174
DB 141 MEELGMAPALOPTGAMPAPAFAPORRAGGVIVASHLQSFLEVSRYVLRHLAQP 194

RESULT 4
Q9GUUO PRELIMINARY; PRT; 195 AA.

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AC O9GJUD;
DT 01-MAR-2001 (Tremblrel. 16, Last Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Granulocyte colony-stimulating factor precursor.
GN Name=G-CSF;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
NCBI_TaxID=9685;
RX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=15151548; PubMed=11675019; DOI=10.1016/S0378-1119(01)00575-3;
RA Yamamoto A., Iwata A., Tuchiya K., Katsumata A., Oishi K., Saito T.,
RT Tsujimoto H., Hasegawa A., Ueda S.;
RT "Molecular cloning and expression of the cDNA encoding feline
RT granulocyte colony-stimulating factor.";
RL Gene 274:263-269 (2001).
DR EMBL; AB042553; BAB17789.1; -.
DR EMBL; AB042553; BAB17789.1; -.
DR HSSP; P35834; 1BGE.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:Cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6.
DR PRODOM; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 195 AA; 21255 MW; 544C682909412FCF CRC64;

Query Match 83.0%; Score 744; DB 2; Length 195;
Best Local Similarity 81.0%; Pred. No. 4,2e-60;
Matches 141; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLLKCEQVRKIQGDAALQEKLCATYKLCHEPELVLLGHSIGIPMAP 60
DB 22 TPLGPASSLPQSFLLKCEQVRKIQGDAALQEKLCATYKLCHEPELVLLGHSIGIPMAP 81
QY 61 LSSCPQALQALQCLQSLHSGFLFYQGLQALLEGISPELGPTLDTQLDVADPATIIMQ 120
DB 82 LSSCPQALQALQCLQSLHSGFLFYQGLQALLEGISPELGPTLDTQLDVADPATIIMQ 141
QY 121 MEELGAPALQPTQGAMPAPAFAPQRRAGGVVASHLSGFLEVSRYVRLHIAOP 174
DB 142 MEDVGAPAVPPTQGTMPFTSAFORRAGGVVASHLSGFLEVSRYVRLHIAOP 195

RESULT 5
CSF3 SHEEP STANDARD; PRT; 174 AA.
AC 028746;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Granulocyte colony-stimulating factor (G-CSF).
GN Name=CSF3;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
NCBI_TaxID=9940;
RX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95102116; PubMed=7528579;

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RA O'Brien P.M., Seow H.F., Rochel J.S., Wood P.R.;
RT "Cloning and sequencing of an ovine granulocyte colony-stimulating
RT factor cDNA.";
RL DNA Seq. 4:339-342 (1994).
CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC cytokines that act in hematopoiesis by controlling the production,
CC differentiation, and function of 2 related white cell populations
CC of the blood, the granulocytes and the monocytes-macrophages. This
CC CSF induces granulocytes (by similarity).
CC -1- SUBUNIT: Monomer
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: O-glycosylated (by similarity).
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L07939; AAA68006.1; -.
DR PIR; T10268; T10268.
DR HSSP; P09919; 1RHG.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRODOM; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor.
FT DISULFID 36 42 By similarity.
FT DISULFID 64 74 By similarity.
FT CARBOHYD 133 133 O-linked (GalNAc...) (By similarity).
SQ SEQUENCE 174 AA; 18806 MW; BASAAB8FD23ACD1E CRC64;

Query Match 82.4%; Score 738; DB 1; Length 174;
Best Local Similarity 82.2%; Pred. No. 1,3e-59;
Matches 143; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLLKCEQVRKIQGDAALQEKLCATYKLCHEPELVLLGHSIGIPMAP 60
DB 1 TPLGPASSLPQSFLLKCEQVRKIQGDAALQEKLCATYKLCHEPELVLLGHSIGIPMAP 60
QY 61 LSSCPQALQALQCLQSLHSGFLFYQGLQALLEGISPELGPTLDTQLDVADPATIIMQ 120
DB 61 LSSCPQALQALQCLQSLHSGFLFYQGLQALLEGISPELGPTLDTQLDVADPATIIMQ 120
QY 121 MEELGAPALQPTQGAMPAPAFAPQRRAGGVVASHLSGFLEVSRYVRLHIAOP 174
DB 121 MEDVGAPAVPPTQGTMPFTSAFORRAGGVVASHLSGFLEVSRYVRLHIAOP 174

RESULT 6
CSF3 CANFA STANDARD; PRT; 175 AA.
AC P35834;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Granulocyte colony-stimulating factor (G-CSF).
GN Name=CSF3;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
RX [1]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=94076341; PubMed=7504736;
RX Lovejoy B., Cascio D., Eisenberg D.;

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RT "Crystal structure of canine and bovine granulocyte-colony stimulating factor (G-CSF).".

RT J. Mol. Biol. 234:640-653 (1993).

CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are cytokines that act in hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages. This CSF induces granulocytes.

CC -1- SUBUNIT: Monomer.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- PTM: O-glycosylated.

CC -1- SIMILARITY: Belongs to the IL-6 superfamily.

DR PDB: 1BGD; X-ray; @=1-175.

DR PDB: 1BGE; X-ray; A/B=1-175.

DR InterPro: IPR009079; 4 helix cytokine.

DR InterPro: IPR003629; GCSF_MGF.

DR InterPro: IPR003573; IL6_MGF_GCSF.

DR Pfam: PF00489; IL6; 1.

DR PRINTS: PR00433; IL6GCSFMGF.

DR PRODOM: PD008388; GCSF_MGF; 1.

DR SMART: SM00126; IL6; 1.

DR PROSITE: PS00254; INTERLEUKIN_6; 1.

KW 3D-structure; Cytokine; Glycoprotein; Growth factor.

FT DISULFID 37 43

FT CARBOHYD 65 75

FT STRAND 134 134 O-linked (GalNAc. .) (By similarity).

FT HELIX 10 10

FT HELIX 12 39

FT HELIX 45 55

FT TURN 56 56

FT HELIX 63 65

FT TURN 67 69

FT HELIX 72 92

FT TURN 93 95

FT TURN 98 100

FT HELIX 101 125

FT TURN 126 126

FT HELIX 144 171

FT TURN 172 172

FT STRAND 173 173

SQ SEQUENCE 175 AA; 18858 MW; 28C26B24990C6DB3 CRC64;

Query Match 81.9%; Score 724; DB 1; Length 175;
Best Local Similarity 80.9%; Pred. No. 3,1e-59;
Matches 140; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 2 PLGPAASSLPQSFLLKLEQVARKIQGDGALQEKLCATYKLCPEELVILGHSIGIPMAPL 61

DB 3 PLGPTGLPQSFLLKLEQVARKIQGDGALQEKLCATYKLCPEELVILGHSIGIPMAPL 62

QY 62 SSCPSQALQIAGCLSQLHSGFLVYQGLQALLEGISPELGPPTLDLQDVADPATTIWOQ 121

DB 63 SSCPSQALQIAGCLSQLHSGFLVYQGLQALLEGISPELGPPTLDLQDVADPATTIWOQ 122

QY 122 BELGMAPALQPTQGMAMPAPASAFORRAGGVIVASHQSFLEVSXVRLHQAQ 174

DB 123 EDLGMAPAVPPTQGMAMPAPASAFORRAGGVIVASHQSFLEVSXVRLHQAQ 175

RESULT 7

CSF3_BOVIN STANDARD; PRT; 195 AA.

AC P35833; O9TV89; Rel. 29, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Granulocyte colony-stimulating factor precursor (G-CSF).

GN Name=CSF3; Synonyms=GCSF;

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

OX NCBI_Taxid=9913;

RM [1] SEQUENCE FROM N.A.

RP STRAIN=Holstein;

RA Helard M., Kehrl M.B. Jr.;

RT "Cloning, sequencing, and analysis of cDNA encoding bovine granulocyte colony stimulating factor.";

RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

RM [2]

RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).

RX MEDLINE=94076341; PubMed=7504736;

RA Lovejoy B., Cascio D., Eisenberg D.;

RT "Crystal structure of canine and bovine granulocyte-colony stimulating factor (G-CSF).".

RT J. Mol. Biol. 234:640-653 (1993).

CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are cytokines that act in hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages. This CSF induces granulocytes.

CC -1- SUBUNIT: Monomer.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- PTM: O-glycosylated.

CC -1- SIMILARITY: Belongs to the IL-6 superfamily.

CC -----

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CC -----

DR EMBL: AF092533; AAD16102.1; -

DR PDB: 1BGC; X-ray; @=2-195.

DR InterPro: IPR003079; 4 helix cytokine.

DR InterPro: IPR003629; GCSF_MGF.

DR InterPro: IPR003573; IL6_MGF_GCSF.

DR Pfam: PF00489; IL6; 1.

DR PRINTS: PR00433; IL6GCSFMGF.

DR PRODOM: PD008388; GCSF_MGF; 1.

DR SMART: SM00126; IL6; 1.

DR PROSITE: PS00254; INTERLEUKIN_6; 1.

KW 3D-structure; Cytokine; Glycoprotein; Growth factor; Signal.

FT SIGNAL 1 21

FT CHAIN 22 195 Granulocyte colony-stimulating factor.

FT DISULFID 57 63

FT CARBOHYD 85 95

FT CONFLICT 93 94

FT HELIX 32 60

FT HELIX 65 69

FT TURN 70 71

FT HELIX 72 75

FT TURN 76 76

FT HELIX 83 85

FT TURN 87 89

FT HELIX 92 112

FT TURN 113 115

FT TURN 118 120

FT HELIX 121 145

FT TURN 164 191

FT HELIX 192 192

FT TURN 192 192

SQ SEQUENCE 195 AA; 21431 MW; 8C06119E4ADFBA73 CRC64;

Query Match 81.1%; Score 727; DB 1; Length 195;
Best Local Similarity 81.0%; Pred. No. 1,5e-58;
Matches 141; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 1 TPLGPAASSLPQSFLLKLEQVARKIQGDGALQEKLCATYKLCPEELVILGHSIGIPMAP 60

DB 22 TPLGPAASSLPQSFLLKLEQVARKIQGDGALQEKLCATYKLCPEELVILGHSIGIPMAP 81

QY 61 LSSCPQALQIAGCLSQLHSGFLVYQGLQALLEGISPELGPPTLDLQDVADPATTIWOQ 120

Db 82 LSSSSSGLQITSLGNGHGLFLYOGLLQALAGISPELAPDTLTDLDVDFATNTMLQ 141
 QY 121 MEELGMAPALOPTGAMPAPASAFORRAGVYVASHQSFLVSVRYRLHIAOP 174
 Db 142 MEDGAPAPVOPPTGAMPFTSAFORRAGVYVASHQSFLVSVRYRLHIAOP 195

RESULT 8

CSF3_PIG STANDARD; PRT; 195 AA.
 ID CSF3_PIG 002837; 019180;
 AC 002837; 019180; (Rel. 36, Created)
 DT 15-JUN-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Granulocyte colony-stimulating factor precursor (G-CSF).
 GN Name=CSF3;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 NC NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP TISSUE=Liver;
 RC GLOSTER S.E., Sandeman R.M., Strom A.D.G.;
 RA "Cloning of a cDNA and gene encoding porcine granulocyte-colony
 RT stimulating factor";
 RT Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
 CC cytokines that act in hematopoiesis by controlling the production,
 CC differentiation, and function of 2 related white cell populations
 CC of the blood, the granulocytes and the monocytes-macrophages. This
 CC CSF induces granulocytes (By similarity).
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: O-glycosylated (By similarity).
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
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 CC
 CC EMBL: Y10494; CAA7518.1; -;
 CC EMBL: U68482; AAB70701.1; -;
 CC EMBL: U68481; AAB70700.1; -;
 CC HSSP: P09919; 1RHG.
 CC InterPro: IPR009079; 4_helix_cytokine.
 CC InterPro: IPR003629; GCSF_MGF.
 CC InterPro: IPR003573; IL6_MGF_GCSF.
 CC Pfam: PF00469; IL6; 1.
 CC PRINTS: PR00433; IL6GCSFMGF.
 CC PRODOM: PD008388; GCSF_MGF; 1.
 CC SMART: SM00126; IL6; 1.
 CC PROSITE: PS00254; INTERLEUKIN_6; 1.
 CC KMW Cytokine; Glycoprotein; Growth factor; Signal.
 CC SIGNAL 1 21 Potential.
 CC FT CHAIN 22 195 Granulocyte colony-stimulating factor.
 CC FT DISULFID 57 63 By similarity.
 CC FT DISULFID 85 95 By similarity.
 CC FT CARBOHYD 154 154 O-linked (GalNAc...) (By similarity).
 CC FT CONFLICT 123 123 A -> R (in Ref. 1).
 CC SO SEQUENCE 195 AA; 21214 MW; 84787F20DB08EA1C CRC64;

Query Match 78.3%; Score 702; DB 1; Length 195;
 Best Local Similarity 79.2%; Pred. No. 3e-56;

Matches 137; Conservative 11; Mismatches 25; Indels 0; Gaps 0;

QY 2 PLGPASSLPQSFLLKLCLEOVKRIQGDPAALQKELCATYKCHPEELVILGSHSIGIPWAPL 61
 Db 23 PLSPASSLPQSFLLKLCLEOVKRIQGDPAALQKELCATYKCHPEELVILGSHSIGIPWAPL 82
 QY 62 SSCPSQALQITGCLNGHGLFLYOGLLQALAGISPELAPDTLTDLDVDFATNTMLQ 121
 Db 83 SSCPSQALQITGCLNGHGLFLYOGLLQALAGISPELAPDTLTDLDVDFATNTMLQ 142
 QY 122 MEELGMAPALOPTGAMPAPASAFORRAGVYVASHQSFLVSVRYRLHIAOP 174
 Db 143 EDLRMAPASLPOTGVTPTSAFORRAGVYVASHQSFLVSVRYRLHIAOP 195

RESULT 9

CSF3_MOUSE STANDARD; PRT; 208 AA.
 ID CSF3_MOUSE 00920;
 AC 00920;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Granulocyte colony-stimulating factor precursor (G-CSF).
 GN Name=CsF3; Synonyms=Csf3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=87017003; PubMed=3489940;
 RX Teuchiya M., Amano S., Kaziro Y., Nagata S.;
 RT "Isolation and characterization of the cDNA for murine granulocyte
 RT colony-stimulating factor";
 RT Proc. Natl. Acad. Sci. U.S.A. 83:7633-7637(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87190474; PubMed=3494605;
 RA Teuchiya M., Kaziro Y., Nagata S.;
 RT "The chromosomal gene structure for murine granulocyte colony-
 RT stimulating factor";
 RT Eur. J. Biochem. 165:7-12(1987).
 RN [3]
 RP PARTIAL SEQUENCE.
 RX PubMed=3501294;
 RA Simpson R.J., Nice E.C., Nicola N.A.;
 RT "Structural studies on the murine granulocyte colony-stimulating
 RT factor";
 RT Biol. Chem. Hoppe-Seyler 368:1327-1331(1987).
 CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
 CC cytokines that act in hematopoiesis by controlling the production,
 CC differentiation, and function of 2 related white cell populations
 CC of the blood, the granulocytes and the monocytes-macrophages. This
 CC CSF induces granulocytes.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: O-glycosylated (By similarity).
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
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 CC
 CC EMBL: M13926; AAA37672.1; -;
 CC EMBL: X05402; CAA28986.1; -;
 CC PIR: A29536; A26496.
 CC HSSP: P09919; 1RHG.
 CC MGD; MGI:1339751; Csf3.
 CC InterPro: IPR009079; 4_helix_cytokine.

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DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Direct protein sequencing; Glycoprotein; Growth factor;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 208 Granulocyte colony-stimulating factor.
FT DISULFID 72 78 By similarity.
FT DISULFID 100 110 O-linked (GalNAc...) (By similarity).
FT CARBOHYD 169 169
SQ SEQUENCE 208 AA; 22421 MW; 0BF3622135C906DB CRC64;

Query Match 71.5%; Score 641; DB 1; Length 208;
Best Local Similarity 75.9%; Pred. No. 1.2e-50;
Matches 129; Conservative 9; Mismatches 32; Indels 0; Gaps 0;

Qy 3 LGPASPLOSFLKLEQVRKIQGDGALQEXLCATYKLCHEBELVLGSHSIGIPWAPIS 62
Db 39 LPPSLPLPRSFLLKSELEQVRKIQAGSVLEQLCATYKLCHEBELVLGSHSIGIPWAPIS 98
Qy 63 SCPSQALQAGLSQHSGLFLYQGLQLQALGSISELGPTLDTLQDVADPATTIWOQME 122
Db 99 GCSQALQOQTCLSLHSGFLFYQGLQLQALGSISELGPTLDTLQDVADPATTIWOQME 158
Qy 123 ELGNAPALOPTGAMPAPAFASAFORRAGVLAASHQSFLEVSRYVLRHIA 172
Db 159 NLGVAPVPTQSTWPTFTSAFORRAGVLAISYLGFLFETRLALHHLA 208

RESULT 10
P97712 PRELIMINARY; PRT; 214 AA.
ID P97712
AC P97712;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Granulocyte colony stimulating factor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97074656; PubMed=8917083; DOI=10.1016/0378-1119(96)00131-X;
RA Han S.W., Ramesh N., Osborne W.R.;
RT "Cloning and expression of the cdna encoding rat granulocyte colony-
stimulating factor.";
RL Gene 175:101-104(1996).
DR EMBL; U73101; AAC52915.1; -.
DR PIR; JC5043; JCS043.
DR HSSP; P08919; IRHG.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 214 AA; 23659 MW; 29BB88B17B64C55 CRC64;

Query Match 70.8%; Score 634; DB 2; Length 214;
Best Local Similarity 73.8%; Pred. No. 5.6e-50;
Matches 127; Conservative 10; Mismatches 35; Indels 0; Gaps 0;

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Qy 3 LGPASPLOSFLKLEQVRKIQGDGALQEXLCATYKLCHEBELVLGSHSIGIPWAPIS 62
Db 30 LPPSLPLPRSFLLKSELEQVRKIQANTLLEQLCATYKLCHEBELVLGSHSIGIPWAPIS 89
Qy 63 SCPSQALQAGLSQHSGLFLYQGLQLQALGSISELGPTLDTLQDVADPATTIWOQME 122
Db 90 SCSSQALQOQTCLSLHSGFLFYQGLQLQALGSISELGPTLDTLQDVADPATTIWOQME 149
Qy 123 ELGNAPALOPTGAMPAPAFASAFORRAGVLAASHQSFLEVSRYVLRHIA 174
Db 150 NLGVAPVPTQSTWPTFTSAFORRAGVLAISYLGFLFETRLALHHLPR 201

RESULT 11
Q9MKR0 PRELIMINARY; PRT; 127 AA.
ID Q9MKR0
AC Q9MKR0;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Granulocyte colony-stimulating factor.
GN Name=G-CSF;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Notonha L.E., Takafuji V.A., Sharova L.V., Crisman M.V., Howard R.D.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF503365; AAM34205.1; -.
DR HSSP; P35833; IBGC.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 127 AA; 13657 MW; 25559C2569802077 CRC64;

Query Match 57.0%; Score 511; DB 2; Length 127;
Best Local Similarity 79.5%; Pred. No. 5.9e-39;
Matches 101; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

Qy 48 VLHGSHIGIPWAPISSCPSQALQAGLSQHSGLFLYQGLQLQALGSISELGPTLDTLQ 107
Db 1 MLHGSHIGIPWAPISSCPSQALQAGLSQHSGLFLYQGLQLQALGSISELGPTLDTLQ 60
Qy 108 LDVADPATTIWOQMEELGNAPALOPTGAMPAPAFASAFORRAGVLAASHQSFLEVSRYV 167
Db 61 LDVADPATTIWOQMEDLVAPVPTFTGMPFTFASAFORRAGVLAASHQSFLEVSRYV 120
Qy 168 LRLHIAOP 174
Db 121 LRYLAEP 127

RESULT 12
MGF_CHICK STANDARD; PRT; 201 AA.
ID MGF_CHICK
AC P13854;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Myelomonocytic growth factor precursor (MGF).
OS Gallus gallus (Chicken).

```


CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89231616; PubMed=2785450;
 RA Leutz A., Damm K., Sternack E., Kowenz E., Nees S., Frank R.,
 RA Gausepohl H., Pan Y.-C.E., Smart J., Hayman M., Graf T.;
 RT "Molecular cloning of the chicken myelomonocytic growth factor (CMGF)
 RT reveals relationship to Interleukin 6 and granulocyte colony
 RT stimulating factor."
 RL EMO J. 8:175-181(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92195319; PubMed=1549124;
 RA Sternack E., Blatter C., Graf T., Leutz A.;
 RT "Structure of the chicken myelomonocytic growth factor gene and
 RT specific activation of its promoter in avian myelomonocytic cells by
 RT protein kinases."
 RL Mol. Cell. Biol. 12:1728-1735(1992).
 CC -1- FUNCTION: Hematopoietic growth factor that stimulates the
 CC proliferation and colony formation of normal and transformed avian
 CC cells of the myeloid lineage.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC -----
 CC EMBL; M85034; AAA48694.1; -;
 CC EMBL; X14477; CAA32639.1; -;
 CC PIR; A42247; 1A2247.
 CC HSSP; P09919; 1RHG.
 DR InterPro: IPR006079; 4 helix cytokine.
 DR InterPro: IPR003629; GCSF_MGF.
 DR InterPro: IPR003573; IL6_MGF_GCSF.
 DR InterPro: IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR ProDom; PD008388; GCSF_MGF; 1.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR GlycoProtein; Growth factor; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 201
 FT DISULFID 61 67
 FT DISULFID 89 99
 FT CARBOHYD 123 123
 FT CARBOHYD 137 137
 SEQUENCE 201 AA; 22373 MW; 240ABDD21B4244A6 CRC64;
 SQ
 Query Match 33.9%; Score 304; DB 1; Length 201;
 Best Local Similarity 40.6%; Pred. No. 9.1e-20;
 Matches 67; Conservative 28; Mismatches 68; Indels 2; Gaps 1;
 QY 11 QSTLKLCEVRYKIOGDGALOEKLCATYKLCHEBEVLVLLGHSIGIWPALSSPSQALQ 70
 DB 36 QFLHNKLEPTKIRKIRGVALLQRAVCTPFLCTEEELQVLQPPPHVLAQPDQCHRRGFQ 95
 QY 71 LAGCLSLHSGSLFLYQGLQALGEGISPELPTLTDTLQDLVADPATTTIWOQMEELGNAPAL 130
 DB 96 AECVCFQIRAGLHAYHDSLGAVALRLLENHTTIVETTLQDLDAANSSNIQQQMEDLGDTVT 155
 QY 131 QPTQ--GAMPAPASAFORRAGGVIVASHLOSFLVSVRYVRLHIAQ 173

DB 156 LPABORSPPPTSGPFOOVGGFFILANFORFLETAYRALRHILAR 200
 RESULT 13
 ID 090Y10 PRELIMINARY; PRT; 241 AA.
 AC 090Y10;
 DT 01-DEC-2001 (TEMBLrel. 19, Created)
 DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
 DT 06-JUN-2004 (TEMBLrel. 27, Last annotation update)
 DE Interleukin-6 precursor.
 GN Name=IL-6;
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schneider K., Klaas R., Kaspers B., Staeheli P.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kaiser P., Rothwell L., Galyov E.E., Barrow P.A., Burnside J.,
 RA Wigley P.;
 RT "Differential cytokine expression in avian cells in response to
 RT invasion by *Salmonella typhimurium*, *Salmonella enteritidis* and
 RT *Salmonella gallinarum*."
 RL Microbiology 146:3217-3226(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kaiser P.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ209540; CAC40812.1; -;
 DR EMBL; AJ250838; CAC15566.2; -;
 DR HSSP; P05231; 1ALU.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR ProDom; PD008388; GCSF_MGF; 1.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 FT SIGNAL 1 47
 FT CHAIN 48 241
 FT SIGNAL 48 241
 FT SIGNAL 48 241
 SEQUENCE 241 AA; 26790 MW; 657F8049F25BD2F8 CRC64;
 SQ
 Query Match 12.4%; Score 111; DB 2; Length 241;
 Best Local Similarity 22.2%; Pred. No. 0.053;
 Matches 46; Conservative 35; Mismatches 74; Indels 52; Gaps 7;
 QY 3 LGPSSLP-----OSFLKCLEQVAKIOGDGALOEKLCATYKLCG 43
 DB 41 LPPAAVPLPAAADSSGVEGLSEBAGARALDCEELANVLDRVAVQDQCKRTVCE 100
 QY 44 PELVLLGSLGIPWAPLSSCPSPALQALG-----CLSLHSGSLFLYQGLQALGEGISPE 98
 DB 101 NSWEMLVRRNNLNP-----KVTEEDGCLLAGPBEKCLTLLSGLFAFYTLERIGTFDS 156
 QY 99 LGPTLDTLQDLVADPATTTIWOQMEELGNAPALQPTOGAMPAPASAFORRAGGVLT----- 152
 DB 157 EKQWNESTCYSTKHLAATIRQNV-----INPEVLP--DSAQKSLANLNSDKWM 206
 QY 153 ---VASHL-----OSFLVSVRYVRLH 171
 DB 207 IKITHMLLRDPTSGFMETKTVAAVRYL 233

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RESULT 14
Q8MJ75 PRELIMINARY; PRT; 212 AA.
AC Q8MJ75;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE IL-6.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee D., Yoo H., Choi I.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF518322; NAM74938.1; -.
DR HSSP; P05231; IADU.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 212 AA; 23881 MW; 1F540E7030BCFD77 CRC64;

Query Match 12.3%; Score 110.5; DB 2; Length 212;
Best Local Similarity 23.3%; Pred. No. 0.052;
Matches 37; Conservative 32; Mismatches 85; Indels 5; Gaps 3;

QY 16 KCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIP-WAPLSSCPQALQLAGCL 74
DB 52 KTEELIKYILKISAMREMECEKYEKSCENSKVLAENNLNLPKMAEKDGCFCGFGNQCETC 111
QY 75 LSGHSGFLYQGLQALBISPELPTLDITLDVADPATTIWOQMBELGNAPALOPT- 133
DB 112 LMRITTYGVLFQIYLDYLOKEYSNKNVAVQISTKALIQTLRQKGNPKDPATTPNPTT 171
QY 134 -QGMPAFAS--AFQBRAGVVLVASHLOSFLVSVYRVR 169
DB 172 NAGLLDKLQSONEMWKNKTITILRSLEDFLOFSIRAIR 210

RESULT 15
Q9XT80 PRELIMINARY; PRT; 208 AA.
AC Q9XT80;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Interleukin 6.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Monodontidae; Delphinapterus.
OC NCBI_Taxid=9749;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20141864; PubMed=10678396; DOI=10.1016/S0165-2427(99)00150-6;
RA St-Laurent G., Archambault D.;
RT "Molecular cloning, phylogenetic analysis and expression of beluga
RT whale (Delphinapterus leucas) interleukin 6.";
RL Vet. Immunol. Immunopathol. 73:31-44(2000).
DR EMBL; AF076643; AAD42929.1; -.
DR HSSP; P05231; IADU.
DR GO; GO:0005576; C:extracellular; IEA.

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DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 208 AA; 23456 MW; 81CC85C6E80389C4 CRC64;

Query Match 12.1%; Score 108; DB 2; Length 208;
Best Local Similarity 21.3%; Pred. No. 0.086;
Matches 33; Conservative 35; Mismatches 81; Indels 6; Gaps 2;

QY 21 VRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIP-WAPLSSCPQALQLAGCLSLQ 79
DB 52 IKYILGKISAMRKEMCEKYDKCENSKALAEENNLNLPKMAEKDGCFCGFGNQCETCLMRIT 111
QY 80 SGLFLYQGLQALBISPELPTLDITLDVADPATTIWOQMBELGNAPALOPTOGA--- 136
DB 112 TGLLEYQIYLDYLONEYEGDKSIEAVQISTKALAQILRQKGNPKDDEVTPPTNNSLM 171
QY 137 -MPAFASAFQBRAGVVLVASHLOSFLVSVYRVR 169
DB 172 NNLOSQNDMMWKNKTITILRSLEDFLOFSIRAIR 206

```

Search completed: July 9, 2005, 12:53:58
Job time : 112.181 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2005, 12:35:24 ; Search time 13.5387 Seconds
(without alignments)
1243.691 Million cell updates/sec

Title: US-10-750-797-2

Perfect score: 901
Sequence: 1 MTPGLPASPSPQSFLLKLE.....SHLOSFLVSVYRLNHLAQP 175

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89.6	99.4	204	1 F0HUGL	granulocyte colony
2	88.4	98.2	207	2 A24573	granulocyte colony
3	74.4	82.6	194	2 T09255	granulocyte colony
4	73.8	81.9	174	2 T10268	granulocyte colony
5	64.2	71.3	208	2 A26496	granulocyte colony
6	63.5	70.5	214	2 JC5043	granulocyte colony
7	30.4	33.7	201	2 A42247	myelomonocytic gro
8	106.5	11.8	212	2 I46590	interleukin 6 - pi
9	106.5	11.8	212	2 I46621	interleukin 6 - pi
10	100	11.1	208	2 T09216	interleukin-6 prec
11	94	10.4	345	2 C82270	hypothetical prote
12	89.5	9.9	2175	1 S03170	homeotic protein c
13	88.5	9.8	666	2 A87577	oligopeptide trans
14	88.5	9.8	786	2 F83292	probable sensor/re
15	86	9.5	208	1 A56610	interleukin-6 prec
16	86	9.5	502	2 I46084	H+-transporting tw
17	85	9.4	207	2 I46084	interleukin 6 - ca
18	84	9.3	274	1 C69362	conserved hypothet
19	83.5	9.3	846	2 JC7721	aryl hydrocarbon r
20	80.5	8.9	406	2 B72766	probable threonyl-
21	80	8.9	474	2 D75550	probable D-alanyl-
22	79.5	8.8	477	2 T46304	hypothetical prote
23	79.5	8.8	351	2 T19623	hypothetical prote
24	79	8.8	423	2 AC3553	4-aminobutyrate tr
25	78	8.7	208	1 S29549	interleukin-6 - sh
26	78	8.7	316	2 H82958	homoserine kinase
27	77.5	8.6	653	2 C82580	oligopeptide trans
28	77	8.5	974	2 AC2076	two-component hybr
29	76.5	8.5	195	2 JH0680	ciliary neurotroph

30	76.5	8.5	506	2 T07942	probable squalene
31	76	8.4	469	2 AD1926	hypothetical prote
32	76	8.4	1704	2 A59188	ATP-binding caset
33	76	8.4	1704	2 S71363	probable ATP-bind
34	75.5	8.4	156	2 J01138	RNA methyltransfe
35	75.5	8.4	3027	2 JQ1917	polyprotein - pars
36	75	8.3	199	1 B38285	interleukin-11 pre
37	75	8.3	219	1 B38285	hypothetical prote
38	75	8.3	245	2 E70583	hypothetical prote
39	75	8.3	472	2 A70951	hypothetical prote
40	74.5	8.3	212	1 IYH082	interleukin-6 prec
41	74.5	8.3	254	2 S34724	probable oxidoredu
42	74.5	8.3	920	2 JC7313	aryl hydrocarbon r
43	74	8.2	367	2 I39172	cyclin-dependent k
44	74	8.2	453	2 H87373	hypothetical prote
45	74	8.2	638	2 A36929	virulence regulato

ALIGNMENTS

RESULT 1

FOHUGL

granulocyte colony-stimulating factor precursor - human

N:Alternate names: colony-stimulating factor 3; G-CSF

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1988 #sequence revision 18-Aug-1995 #text_change 09-Jul-2004

C:Accession: A25093; A49796; A47587; S68331

R:Nagata, S.; Tsuchiya, M.; Asano, S.; Yamamoto, O.; Hirata, Y.; Kubota, N.; Oheda, M.;

EMBO J. 5, 575-581, 1986

A>Title: The chromosomal gene structure and two mRNAs for human granulocyte colony-stimulating factor

A:Reference number: A25093; MUID:86220137; PMID:2423327

A:Accession: A25093

A:Molecule type: DNA

A:Residues: 1-204 <NAG>

A:Cross-references: UNIPROT:P09919; EMBL:X03656; EMBL:X03655; NID:g31693; PID:CAA27290

R:Devlin, J.J.; Devlin, P.E.; Myambo, K.; Lilly, M.B.; Rado, T.A.; Warren, M.K.

J. Leukoc. Biol. 41, 302-306, 1987

A>Title: Expression of granulocyte colony-stimulating factor by human cell lines.

A:Reference number: A49796; MUID:87196936; PMID:3494801

A:Accession: A49796

A:Molecule type: mRNA

A:Residues: 1-204 <DEV>

A:Cross-references: GB:M17706; NID:G183040; PID:AAA5882.1; PID:G183041

R:Souza, L.M.; Boone, T.C.; Gabriello, J.; Lai, P.H.; Zeebo, K.M.; Murdoch, D.C.; Chazi

Science 232, 61-65, 1986

A>Title: Recombinant human granulocyte colony-stimulating factor: effects on normal and

A:Reference number: A47587; MUID:86151684; PMID:2420009

A:Accession: A47587

A:Molecule type: mRNA

A:Residues: 15-204 <SOU>

A:Cross-references: GB:M13008; NID:G183044; PID:AAA03056.1; PID:G183045

R:Hantlu, M.; Horan, T.; Arakawa, T.; Le, J.; Katata, V.; Rohde, M.F.

Arch. Biochem. Biophys. 324, 344-356, 1995

A>Title: Extracellular domain of granulocyte-colony stimulating factor receptor.

A:Reference number: S68331; MUID:96133662; PMID:8554326

A:Accession: S68331

A:Molecule type: protein

A:Residues: 'M', 'J', '46' <HAN>

A:Genetics:

A:Gene: GDB:CSF3

A:Cross-references: GDB:119083; OMIM:138970

A:Map position: 17q11.2-17q12

A:Introns: 14/1; 65/3; 101/3; 150/3

C:Function:

A:Description: stimulates the differentiation and proliferation of hematopoietic progen

C:Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-204/Product: granulocyte colony-stimulating factor #status predicted <MAT>

F:66-72,94-104/Disulfide bonds: #status predicted

Query Match 99.4%; Score 896; DB 1; Length 204;
 Best Local Similarity 100.0%; Pred. No. 3,7e-78;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TPGLPASPSPFLKLEQVRKIQGDGAALQEKLCATYKLCHEBELVLLGHSIGIPWAP 61
 DB 31 TPGLPASPSPFLKLEQVRKIQGDGAALQEKLCATYKLCHEBELVLLGHSIGIPWAP 90
 QY 62 LSSCPSPQALQAGLSQHSGLFLYQGLQALGSPISPELPTDPTLDVADPATTTTMOQ 121
 DB 91 LSSCPSPQALQAGLSQHSGLFLYQGLQALGSPISPELPTDPTLDVADPATTTTMOQ 150
 QY 122 MEELGNAPALQPTQGAMPAPAFASAFORRAGVTVASHLOSFLVSVYRLRLAQP 175
 DB 151 MEELGNAPALQPTQGAMPAPAFASAFORRAGVTVASHLOSFLVSVYRLRLAQP 204

RESULT 2

A24573
 granulocyte colony-stimulating factor precursor variant splice form CHU-2 - human

N;Alternate names: colony-stimulating factor 3; G-CSF
 C;Species: Homo sapiens (man)
 C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
 C;Accession: A24573
 R;Negata, S.; Tsuchiya, M.; Asano, S.; Kaziro, Y.; Yamazaki, T.; Yamamoto, O.; Hirata, Y.
 Nature 319, 415-418, 1986
 A;Title: Molecular cloning and expression of cDNA for human granulocyte colony-stimulating factor.
 A;Reference number: A24573; MUID:86118679; PMID:3484805
 A;Molecule type: mRNA
 A;Residues: 1-207 <N>G>
 A;Cross-references: UNIPROT:P09919; EMBL:X03438; NID:G31689; PIDN:CAA27168.1; PID:G31690
 C;Comment: This variant splice form is not expressed in three other cell lines and may be a gene.
 C;Genetics:
 A;Gene: GDB:CSF3
 A;Cross-references: GDB:119083; OMIM:138970
 A;Map position: 17q11.2-17q12
 A;Intons: 14/1; 68/3; 104/3; 153/3
 C;Superfamily: Interleukin-6
 C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer
 F;1-30/Domain: signal sequence #status predicted <SIG>
 F;31-207/Product: granulocyte colony-stimulating factor variant splice form CHU-2 #status predicted
 F;69-75,97-107/Disulfide bonds: #status predicted

Query Match 98.2%; Score 884.5; DB 2; Length 207;
 Best Local Similarity 98.3%; Pred. No. 4.7e-77;
 Matches 174; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 2 TPGLPASPSPFLKLEQVRKIQGDGAALQEKLCATYKLCHEBELVLLGHSIGIP 58
 DB 31 TPGLPASPSPFLKLEQVRKIQGDGAALQEKLCATYKLCHEBELVLLGHSIGIP 90
 QY 59 WAPLSPSPQALQAGLSQHSGLFLYQGLQALGSPISPELPTDPTLDVADPATTTI 118
 DB 91 WAPLSPSPQALQAGLSQHSGLFLYQGLQALGSPISPELPTDPTLDVADPATTTI 150
 QY 119 WQMEELGNAPALQPTQGAMPAPAFASAFORRAGVTVASHLOSFLVSVYRLRLAQP 175
 DB 151 WQMEELGNAPALQPTQGAMPAPAFASAFORRAGVTVASHLOSFLVSVYRLRLAQP 207

RESULT 3

T09255
 granulocyte colony-stimulating factor precursor - cat (fragment)

C;Species: Felis silvestris catus (domestic cat)
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C;Accession: T09255
 R;Dunham, S.P.; Onions, D.E.
 submitted to the EMBL Data Library, September 1996
 A;Description: Cloning, sequence and expression of feline granulocyte colony stimulating factor.
 A;Reference number: Z16630
 A;Accession: T09255
 A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA
 A;Residues: 1-194 <DUN>
 A;Cross-references: UNIPROT:O02708; EMBL:Y08558
 C;Function:
 A;Description: stimulates the differentiation and proliferation of hematopoietic progenit

C;Superfamily: Interleukin-6
 C;Keywords: cytokine; growth factor; macrophage
 F;1-20/Domain: signal sequence (fragment) #status predicted <SIG>
 F;21-194/Product: granulocyte colony-stimulating factor #status predicted <MAT>

Query Match 82.6%; Score 744; DB 2; Length 194;
 Best Local Similarity 81.0%; Pred. No. 1.1e-63;
 Matches 141; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 2 TPGLPASPSPFLKLEQVRKIQGDGAALQEKLCATYKLCHEBELVLLGHSIGIPWAP 61
 DB 21 TPGLPASPSPFLKLEQVRKIQGDGAALQEKLCATYKLCHEBELVLLGHSIGIPWAP 80
 QY 62 LSSCPSPQALQAGLSQHSGLFLYQGLQALGSPISPELPTDPTLDVADPATTTTMOQ 121
 DB 81 LSSCPSPQALQAGLSQHSGLFLYQGLQALGSPISPELPTDPTLDVADPATTTTMOQ 140
 QY 122 MEELGNAPALQPTQGAMPAPAFASAFORRAGVTVASHLOSFLVSVYRLRLAQP 175
 DB 141 MEELGNAPALQPTQGAMPAPAFASAFORRAGVTVASHLOSFLVSVYRLRLAQP 194

RESULT 4

T10268
 granulocyte colony-stimulating factor - sheep (fragment)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C;Accession: T10268
 R;O'Brien, P.M.; Seow, H.F.; Rothel, J.S.; Wood, P.R.
 DNA Seq. 4, 339-342, 1994
 A;Title: Cloning and sequencing of an ovine granulocyte colony-stimulating factor cDNA.
 A;Reference number: Z17009; MUID:95102116; PMID:7528579
 A;Accession: T10268
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-174 <OR>
 A;Cross-references: UNIPROT:Q28746; EMBL:L07939; NID:G310381; PIDN:AAA68006.1; PID:G3103
 C;Genetics:
 A;Gene: CSF
 A;Function:
 A;Description: stimulates the differentiation and proliferation of hematopoietic progenit
 C;Superfamily: Interleukin-6
 C;Keywords: cytokine; growth factor; macrophage

Query Match 81.9%; Score 738; DB 2; Length 174;
 Best Local Similarity 82.2%; Pred. No. 3.7e-63;
 Matches 143; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

QY 2 TPGLPASPSPFLKLEQVRKIQGDGAALQEKLCATYKLCHEBELVLLGHSIGIPWAP 61
 DB 1 TPGLPASPSPFLKLEQVRKIQGDGAALQEKLCATYKLCHEBELVLLGHSIGIPWAP 60
 QY 62 LSSCPSPQALQAGLSQHSGLFLYQGLQALGSPISPELPTDPTLDVADPATTTTMOQ 121
 DB 61 LSSCPSPQALQAGLSQHSGLFLYQGLQALGSPISPELPTDPTLDVADPATTTTMOQ 120

QY 122 MEELGNAPALQPTQGAMPAPAFASAFORRAGVTVASHLOSFLVSVYRLRLAQP 175
 DB 121 MEELGNAPALQPTQGAMPAPAFASAFORRAGVTVASHLOSFLVSVYRLRLAQP 174

RESULT 5

A26496
 granulocyte colony-stimulating factor precursor - mouse

N;Alternate names: G-CSF
 C;Species: Mus musculus (house mouse)
 C;Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 09-Jul-2004
 C;Accession: A26496; S02493

R.Tsuchiya, M.; Kaziro, Y.; Nagata, S.
Eur. J. Biochem. 165, 7-12, 1987
A:Title: The chromosomal gene structure for murine granulocyte colony-stimulating factor
A:Reference number: A29536, MUID:87190474; PMID:3494605
A:Accession: A29536
A:Molecule type: DNA
A:Residues: 1-208 <TS2>
A:Cross-references: UNIPROT:P09920; GB:X05402; NID:G51059; PIDN:CAA28986.1; PID:G51060
R:Tsuchiya, M.; Asano, S.; Kaziro, Y.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 83, 7633-7637, 1986
A:Title: Isolation and characterization of the cDNA for murine granulocyte colony-stimulating factor
A:Reference number: A26496, MUID:87017003; PMID:3489940
A:Accession: A26496
A:Molecule type: mRNA
A:Residues: 1-208 <TS2>
A:Cross-references: GB:M13926; NID:G193451; PIDN:AAA7672.1; PID:G309248
R:Simpeon, R.J.; Nice, E.C.; Nicols, N.A. 1987
Biol. Chem. Hoppe-Seyler 368, 1327-1331, 1987
A:Title: Structural studies on the murine granulocyte colony-stimulating factor.
A:Reference number: S02493; MUID:88106998; PMID:3501294
A:Accession: S02493
A:Status: preliminary
A:Status: preliminary
A:Molecule type: protein
A:Residues: 31-34, 'X', 36-43, 48-51, 'X', 53-57, 'X', 60-71, 159-164, 'X', 166-176, 183-198, 'X', 200-201
C:Genetics:
A:introns: 14/1; 71/3; 107/3; 156/3
C:Superfamily: interleukin-6
C:Keywords: cytokine; growth factor; macrophage; monomer

Query Match 71.3%; Score 642; DB 2; Length 208;
Best Local Similarity 74.6%; Pred. No. 6.7e-54;
Matches 129; Conservative 11; Mismatches 33; Indels 0; Gaps 0;

Qy 1 MTPIGPASLPSQFLKLEQVRKIQGDAALQEKLCATYKCHPEBVLVLSHSIGIPWA 60
Db 36 VSALPSPSLPSPFLKLSLEQVRKIQASGSVLEQLCATYKCHPEBVLVLSHSIGIPWA 95
Qy 61 PLSSCPQALQAGLSQLHSGFLFYQGLQLALLEGISPELGTLDLQDVADFAFTTIWQ 120
Db 96 SLSSGSSQALQOTQGLSLHSGFLFYQGLQLALLEGISPELGTLDLQDVADFAFTTIWQ 155

Qy 121 QMEBGMAPALQPTQGAMPAPAFASAFORRAGVLAASHQSFLEVSRYLRHLAQ 173
Db 156 QMENIGVAPVQPTQGAMPAPAFASAFORRAGVLAASHQSFLEVSRYLRHLAQ 208

RESULT 6
UC5043
granulocyte colony-stimulating factor precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C:Accession: UC5043
R:Han, S.W.; Ramesh, N.; Osborne, W.R.A.
Gene 175, 101-104, 1996
A:Title: Cloning and expression of the cDNA encoding rat granulocyte colony-stimulating factor
A:Reference number: JC5043; MUID:97074656; PMID:8917083
A:Accession: JC5043
A:Molecule type: mRNA
A:Residues: 1-214 <HAN>
A:Cross-references: UNIPROT:P97712; GB:U37101; NID:G168068; PIDN:AA252915.1; PID:G168068
A:Experimental source: skin fibroblasts
C:Comment: This receptor acts on precursor hemopoietic cells to control the production of interleukin-6
F:1-21/Domin: signal sequence #status predicted <SIG>
F:22-214/Product: granulocyte colony-stimulating factor #status predicted <MAT>

Query Match 70.5%; Score 635; DB 2; Length 214;
Best Local Similarity 72.6%; Pred. No. 3.2e-53;
Matches 127; Conservative 12; Mismatches 36; Indels 0; Gaps 0;

Qy 1 MTPIGPASLPSQFLKLEQVRKIQGDAALQEKLCATYKCHPEBVLVLSHSIGIPWA 60
Db 27 VSLPSPSLPSPFLKLSLEQVRKIQANTELLEQLCATYKCHPEBVLVLSHSIGIPKA 86

Qy 61 PLSSCPQALQAGLSQLHSGFLFYQGLQLALLEGISPELGTLDLQDVADFAFTTIWQ 120
Db 87 SLSSGSSQALQOTQGLSLHSGFLFYQGLQLALLEGISPELGTLDLQDVADFAFTTIWQ 146

Qy 121 QMEBGMAPALQPTQGAMPAPAFASAFORRAGVLAASHQSFLEVSRYLRHLAQ 175
Db 147 QMENIGVAPVQPTQGAMPAPAFASAFORRAGVLAASHQSFLEVSRYLRHLAQ 201

RESULT 7
A42247
myelomonocytic growth factor precursor - chicken
N:Alternate names: colony-stimulating factor CMGF
C:Species: Gallus gallus (chicken)
C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A42247; S03633
R:Sternneck, E.; Blatter, C.; Graf, T.; Leutz, A.
Mol. Cell. Biol. 12, 1728-1735, 1992
A:Title: Structure of the chicken myelomonocytic growth factor gene and specific active site
A:Reference number: A42247; MUID:92195319; PMID:1549124
A:Accession: A42247
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-201 <STE>
A:Cross-references: UNIPROT:P13854
A:Note: sequence extracted from NCBI backbone (NCBI:89832, NCBI:P13854)
R:Leutz, A.; Damm, K.; Sternneck, E.; Kowenz, E.; Nees, S.; Frank, R.; Gausepohl, H.; Pa
EMBO J. 8, 175-181, 1989
A:Title: Molecular cloning of the chicken myelomonocytic growth factor (CMGF) reveals a
A:Reference number: S03633; MUID:892331616; PMID:2785450
A:Accession: S03633
A:Molecule type: mRNA
A:Residues: 1-201 <LEU>
A:Cross-references: EMBL:X14477; NID:G63596; PIDN:CAA32639.1; PID:G63597
C:Superfamily: interleukin-6
C:Keywords: glycoprotein
F:1-23/Domin: signal sequence #status predicted <SIG>
F:24-201/Product: myelomonocytic growth factor #status predicted <MAT>
F:123/13/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 33.7%; Score 304; DB 2; Length 201;
Best Local Similarity 40.6%; Pred. No. 1.2e-21;
Matches 67; Conservative 28; Mismatches 68; Indels 2; Gaps 1;

Qy 12 QSLFKLEQVRKIQGDAALQEKLCATYKCHPEBVLVLSHSIGIPAPSSCSQALQ 71
Db 36 QLFHKNLEFTRKIRGDVAALQRAVCDPQLCTEEBQLVQDPDHLVQAPLDQCHKRGFQ 95

Qy 72 LAGLSQLHSGFLFYQGLQLALLEGISPELGTLDLQDVADFAFTTIWQMEBGMAPAL 131
Db 96 AEVCFQTRAGLHAHDSLSGLAVLRLPHTTTLVETLQDANLSSNTQQQMEBGLDVT 155

Qy 132 QPTQ-GAMPAPAFASAFORRAGVLAASHQSFLEVSRYLRHLAQ 174
Db 156 LPARQRPPTPSPFPQOQVGGFFILANPQRFLETATRALRHLAR 200

RESULT 8
I46590
interleukin 6 - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: I46590
R:Mathialagan, N.; Bixby, J.; Roberts, M.R.
Mol. Reprod. Dev. 32, 324-330, 1992
A:Title: Expression of interleukin-6 in porcine, ovine, and bovine preimplantation conc
A:Reference number: I46590; MUID:92360284; PMID:1497880
A:Accession: I46590
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-212 <MAT>
A:Cross-references: UNIPROT:P26893; GB:M80258; NID:G164514; PIDN:AA27127.1; PID:G16451

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:886-958/Domain: cut repeat homology <CU1>
F:1339-1411/Domain: cut repeat homology <CU2>
F:1617-1689/Domain: cut repeat homology <CU3>
F:1746-1802/Domain: homeobox homology <HOX>

Query Match	9.9%	Score 89.5;	DB 1;	Length 2175;
Best Local Similarity	23.8%;	Pred. No. 6.7;		
Matches 35;	Conservative 20;	Mismatches 61;	Indels 31;	Gaps 3

```

QY      28  GGALLOEGLCTATYKLCHEEELVILGSLGIPAPAPSSCSQALQLAGCLSGLSGFLVQ  87
D5      1404  DENAVHKLVASQYKIA-PEKLMRTSYSSSPMP-----Q  143
QY      88  GLLQALEGISPELGPTLDPTLOLDVADFATTIMQOMEELGMAPALPTOGAMPAPASAFOR  147
D5      1438  GLASRMQALASLPQMQRMSSELKIQEAPRAQOHTLMQOMAAAMSAAMQOOQ-----VAQAOQO  149
QY      148  RAGGVLVASHLQSELEVSRYVRLHLDAQ  174
D5      1493  AQAQAQAQOQHLOQAQAQOHLQOQOQHLLAQ  1519

```

RESULT 13

C/Accession: A87577
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C/Nieman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Leub, M.C.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Klotzel, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of *Caulobacter crescentus*.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: A87577
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-666 <570>
A/Cross-references: UNIPROT:Q9A523; GB:AB005673; NID:g13424225; PIDN:AAK24613.1; GSPDB:C/C/Gene: CC2646
C/Gene: CC2646
Superfamily: *Pyrococcus horikoshii* hypothetical protein PH0361

Query Match	9.8%	Score 88.5;	DB 2;	length 666;
Best Local Similarity	32.5%;	Pred. No. 2;		
Matches 37;	Conservative 14;	Mismatches 48;	Indels 15;	Gaps 4;

QY	51	LGHSIGLPMPLASSCPQALQIACLSQTHSGLFYQOILLALBESISELPITDITD	110
Db	196	LGAASGATGIGASS--SLALMGAGHIMGITVGAMFGLFAMAILVILITLVTPMPEAD	253
QY	111	VADPATINQ-QMEELG-----MAPALDP--TGAMPPAPASAFQRRAGG	151
Db	254	AATHTALTVMSQVREFLGAVIGAAAIWTLATLVGGITSGLSAFAPAAQARRAG	307

RESULT 14

probable sensor/response regulator hybrid PA2824 [imported] - *Pseudomonas aeruginosa* (strain H460) [NC_017292]
C/Specties: *Pseudomonas aeruginosa*
C/SpecDate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: F83392
R/Stover, C.K.; Pham, X.Q.; Errin, A.L.; Micozuchi, S.D.; Warren, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim, J.; Lory, S.; Olsen, M.V.
Nature 406, 959-964, 2000
A/File: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
Reference number: AB2950; MUID:20437337; PMID:10584043

A;Cross-references: UNIPROT:Q91019; GB:AE004709; GB:AE004091; NID:g9948994; PIDN:AA6066
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2824

Query Match	9.8%;	Score 88.5;	DB 2;	Length 786;
Best Local Similarity	29.2%;	Pred. No. 2.4;		
Matches 50; Conservative	19;	Mismatches 49;	Indels 53;	Gaps 10

QY 27 GDGAALOEKIC-ATYKCKHPEELVILIG--HSIGIPMPPLSSCSPOALDAG-CISQLSHG 82

Db 490 GLGLATIRKICEANQOGEITVESTYGLSSLSFVSGLPLAVSP-PIQALDLRGHVIQOCSAN 548

QY 83 LFTYGLGLQALGTSPE-----LGPYLDTLQDVADVFATTIWOQMEIGMA 128

Db 549 -----SGIAQLLIQTWLPKRWGLBYKRLTFDDSLHGSIDLVLISDCPDCL-----MGLR 595

QY 129 PALQPTQGAMPAFASAFQRBAGVGLVASHLOSFL--EVSRYEV--LRHDAQP 175

Db 596 PST-----GTPILLVTANGSFLPEELAKRLSLPELROLARP 629

RESULT 15

interleukin-6 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A56610; S22162
R:Crossmans, L.; Cludts, I.; Cleuter, Y.; Kettmann, R.; Bury, A.
DNA Seq. 2, 411-413, 1992
A:Title: Nucleotide sequence of bovine interleukin-6 cDNA.
A:Reference number: A56610; MUID:93076003; PMID:1446077
A:Accession: A56610
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-208 <DRO>
A:Cross-references: UNIPROT:P26892; EMBL:X57317; NID:G2193; PIDN:CAA40572.1; PID:G2194
A:Experimental source: UNIPROT: induced B cell-lymphosarcoma
A:Note: sequence extracted from NCBI backbone (NCBI:118917)
C:Superfamily: interleukin-6
/:Keywords: cytokine

Query Match	9.54;	Score 86;	DB 1;	Length 208;
Best Local Similarity	20.54;	Pred. No. 0.83;		
Matches	36;	Conservative	37;	Mismatches 95; Indels 8; Gaps 33;

QY 3 PLE----PASIPOSFLIKCLEQ-----VRKIOGDGAALQEKLCATYKCHPEELVLTGSL 55
Db 31 PIGEDFPKNDTTPERLLLTTPTEKTEBALIKRWVDKISARKEICENKDCBSSKETLAENKL 90
QY 56 GIP-WAPLSSCPQALQALGCLLSQMSGLFLYQGLQALSGISPELGPTIDTLODVADF 114
Db 91 NLPKMEKQKCFQSGFNQALCLARTTAGLEGTQIYLDYLONEYEGNOENVDLKNKRTTL 150
QY 115 ATTIIQOMBELGAPALOPTQGMPPASAFQRRAGCVLVASHQSFLEVSYRVLR 170
151 IQILKKKIDLTTPATNTDLEKQSSNEMVWNAKILIRNLNENLQSLRAIR 206

Search completed: July 9, 2005, 12:45:23
Job time : 14.5387 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2005, 12:41:15 ; Search time 111.819 Seconds

(without alignments)
801.415 Million cell updates/sec

Title: US-10-750-797-2

Perfect score: 901
Sequence: 1 MTPGLPASSLPQSFLKCLE.....SHLOSFLEVSRYVRLHQAQ 175

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	896	99.4	200	Q8N4W3	Q8N4W3 homo sapien
2	884.5	98.2	207	CSF3_HUMAN	P09919 homo sapien
3	744	82.6	194	CSF3_PELCA	002708 felis silve
4	744	82.6	195	Q9G4U0	Q9G4U0 felis silve
5	739	82.0	175	CSF3_CANFA	P35834 canis fam11
6	738	81.9	174	CSF3_SHEEP	Q28746 ovis aries
7	727	80.7	195	CSF3_BOVIN	P35833 bos taurus
8	702	77.9	195	CSF3_MOUSE	002837 sus scrofa
9	642	71.3	208	CSF3_MOUSE	P09920 mus musculu
10	635	70.5	214	P97712	P97712 rattus norv
11	511	56.7	127	Q8MKE0	Q8MKE0 equus cabal
12	304	33.7	201	MGF_CHICK	P13854 gallus gall
13	111	12.3	241	Q90Y10	Q90Y10 gallus gall
14	110.5	12.3	212	Q8M775	Q8M775 sus scrofa
15	108	12.0	208	Q9XT80	Q9XT80 delphinape
16	106.5	11.8	212	IL6_PIG	P26893 sus scrofa
17	101	11.2	205	IL6_ORCOR	Q28747 orctinus orc
18	100	11.1	208	IL6_HORSE	Q95181 equus cabal
19	96	10.7	189	Q6N282	Q6N282 homo sapien
20	96	10.7	189	Q9H2A5	Q9H2A5 homo sapien
21	95	10.5	208	IL6_PELCA	P41683 felis silve
22	94.5	10.5	455	Q8D706	Q8D706 vibrio vuln
23	94	10.4	345	Q9KTL6	Q9KTL6 vibrio chol
24	93	10.3	189	Q9NPF7	Q9NPF7 homo sapien
25	91	10.1	202	Q6N280	Q6N280 homo sapien
26	89.5	9.9	214	Q8MKE5	Q8MKE5 sus scrofa
27	89.5	9.9	2175	HMCTU_BROME	P10180 drosophila
28	88.5	9.8	666	Q9A523	Q9A523 caulobacter
29	88.5	9.8	786	Q91019	Q91019 pseudomonas
30	88.5	9.8	1931	Q8RJY3	Q8RJY3 stigmatella
31	88	9.8	290	Q9P0S7	Q9P0S7 homo sapien

32	86	9.5	208	1	IL6_BOVIN	P26892 bos taurus
33	86	9.5	502	2	Q34008	Q34008 beta vulgar
34	86	9.5	788	2	Q8CF87	Q8CF87 mus musculu
35	86	9.5	850	2	Q7TQ21	Q7TQ21 mus musculu
36	86	9.5	851	2	Q8CF88	Q8CF88 mus musculu
37	86	9.5	852	2	Q81179	Q81179 mus musculu
38	85.5	9.5	211	2	Q865W7	Q865W7 camelus bac
39	85.5	9.5	1288	2	Q8LQ88	Q8LQ88 oryza sativ
40	85	9.4	193	2	Q6N2H9	Q6N2H9 sus scrofa
41	85	9.4	208	2	Q6V919	Q6V919 bubalus bub
42	84.5	9.4	209	1	IL6_PHOVI	Q28819 phoca vitul
43	84.5	9.4	211	1	IL6_TAMGL	Q865X6 lama glama
44	84.5	9.4	455	2	Q7MDW7	Q7MDW7 vibrio vuln
45	84	9.3	175	2	Q9YTH4	Q9YTH4 actus nigri

ALIGNMENTS

RESULT 1	ID	Q8N4W3	PRELIMINARY:	PRT:	200 AA.
AC	Q8N4W3				
DT	01-OCT-2002 (TREMBLrel. 22, Created)				
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DE	Colony stimulating factor 3, isoform c.				
GN	Name=CSF3;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_Taxid=9606;				
RP	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Skin;				
RX	MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Ditachenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Cassavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				
RA	Bosch S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villalón D.K., Wuzny D.M., Sodergren E.V., Lu X., Gibbs R.A.,				
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,				
RA	Krzyszinski M.I., Skalska U., Smalusi D.E., Scherch A., Schein J.E.,				
RA	Jones S.J., Marra M.A.,				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Skin;				
RA	Strausberg R.,				
RL	Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.				
DR	EMBL; BC033245; AAH3245.1; -				
DR	HSSP; P09919; IGNC.				
DR	GO; GO:0005576; C:extracellular; IEA.				
DR	GO; GO:0005125; F:cytokine activity; IEA.				
DR	GO; GO:0005138; F:interleukin-6 receptor binding; IEA.				
DR	GO; GO:0006955; P:immune response; IEA.				
DR	InterPro; IPR009079; 4 helix cytokine.				
DR	InterPro; IPR003629; GCSF_MGF.				
DR	InterPro; IPR003573; IL6_MGF_GCSF.				
DR	InterPro; IPR003574; Interleukin_6.				
DR	Pfam; PF00489; IL6; 1.				
DR	PRINTS; PR00433; IL6GCSFMGF.				

DR PRINTS; PR00434; INTERLEUKIN6.
 DR Prodom; PD008388; GCSF MGF; 1.
 DR Prodom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR SMART; PS00254; INTERLEUKIN_6; 1.
 DR SEQUENCE 200 AA; 21543 MW; 8648A55B329A96C CRC64;
 SQ

Query Match 99.4%; Score 896; DB 2; Length 200;
 Best Local Similarity 100.0%; Pred. No. 6.9e-74;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TPLGPPASLPQSFLLKLEQVRKIQGDGALQEKLCATYKLCHEELVLLGSHLGIWPAP 61
 DB 27 TPLGPPASLPQSFLLKLEQVRKIQGDGALQEKLCATYKLCHEELVLLGSHLGIWPAP 86
 QY 62 LSSCPGQALQACLSQSHGLFLYQGLQALBESISELPTLDTLQADVADPATTITWQ 121
 DB 87 LSSCPGQALQACLSQSHGLFLYQGLQALBESISELPTLDTLQADVADPATTITWQ 146

QY 122 MEELGNAPLQPTQGNAPAFAPAFAPORAGGVVAVASHLOFLEVSYRYLRHAAOP 175
 DB 147 MEELGNAPLQPTQGNAPAFAPAFAPORAGGVVAVASHLOFLEVSYRYLRHAAOP 200

RESULT 2
 CSF3_HUMAN STANDARD; PRT; 207 AA.
 ID CSF3_HUMAN P09919;
 AC P09919;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Granulocyte colony-stimulating factor precursor (G-CSF) (Pluripolietin)
 DE (Fligraetm) (lenograetm).
 DE Name=CSF3;
 OS Homo sapiens (human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 *OX
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86118679; PubMed=3484805; Kaziro Y., Yamazaki T., Yamamoto O.,
 RA Nagata S., Tsuchiya M., Asano S., Yamamoto O., Hirata Y., Kubota N.,
 RA Hirata Y., Kubota N., Oheda M., Nomura H., Ono M.;
 RT "Molecular cloning and expression of cDNA for human granulocyte
 RT colony-stimulating factor.";
 RL Nature 319:415-418(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86220137; PubMed=2423327;
 RA Nagata S., Tsuchiya M., Asano S., Yamamoto O., Hirata Y., Kubota N.,
 RA Oheda M., Nomura H., Yamazaki T.;
 RT "The chromosomal gene structure and two mRNAs for human granulocyte
 RT colony-stimulating factor.";
 RL EMBO J. 5:575-581(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87196936; PubMed=3494801;
 RA Devlin J.J., Devlin P.E., Myambo K., Lilly M.B., Rado T.A.,
 RA Warren M.K.;
 RT "Expression of granulocyte colony-stimulating factor by human cell
 RT lines.";
 RL J. Leukoc. Biol. 41:302-306(1987).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANTS MET-157 AND THR-174.
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.-L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RT "Sequences of the human HL66682 program for genomic applications, UW-
 RT FHCC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 19-207 FROM N.A.
 RX MEDLINE=86151684; PubMed=2420009;
 RA Souza L.M., Boone T.C., Gabrilove J., Lai P.H., Zsebo K.M.,

RA Murdock D.C., Chazin V.R., Bruszewski J., Lu H., Chen K.K.,
 RA Barendt J., Platzer E., Moore M.A.S., Mettelmann R., Welte K.;
 RT "Recombinant human granulocyte colony-stimulating factor: effects on
 RT normal and leukemic myeloid cells.";
 RL Science 232:61-66(1986).
 RN [6]
 RP CARBOHYDRATE-LINKAGE SITE.
 RX MEDLINE=93293942; PubMed=7685769;
 RA Clogston C.L., Hu S., Boone T.C., Lu H.S.;
 RT "Glycosidase digestion, electrophoresis and chromatographic analysis
 RT of recombinant human granulocyte colony-stimulating factor glycoforms
 RT produced in Chinese hamster ovary cells.";
 RL J. Chromatogr. A 637:55-62(1993).
 RN [7]
 RP STRUCTURE BY NMR.
 RX MEDLINE=93106200; PubMed=1281794; DOI=10.1016/0014-5793(92)81521-M;
 RA Zink T., Ross A., Ambrosius D., Rudolph R., Holak T.A.;
 RT "Secondary structure of human granulocyte colony-stimulating factor
 RT derived from NMR spectroscopy.";
 RL FEBS Lett. 314:435-439(1992).
 RN [8]
 RP STRUCTURE BY NMR.
 RX MEDLINE=94304859; PubMed=7518249;
 RA Zink T., Ross A., Luehrs K., Cieciar C., Rudolph R., Holak T.A.;
 RT "Structure and dynamics of the human granulocyte colony-stimulating
 RT factor determined by NMR spectroscopy. Loop mobility in a four-helix-
 RT bundle protein.";
 RL Biochemistry 33:8453-8463(1994).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=93281718; PubMed=7685117;
 RA Hill C.P., Oseilund T.D., Eisenberg D.;
 RT "The structure of granulocyte-colony-stimulating factor and its
 RT relationship to other growth factors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:5167-5171(1993).
 CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
 CC cytokines that act in hematopoiesis by controlling the production,
 CC differentiation, and function of 2 related white cell populations
 CC of the blood, the granulocytes and the monocytes/macrophages. This
 CC CSF induces granulocytes.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=long;
 CC IsoId=P09919-1; Sequence=Displayed;
 CC Name=short;
 CC IsoId=P09919-2; Sequence=VSP_002673;
 CC -1- PTM: O-glycan consists of Gal-GalNAc disaccharide which can be
 CC modified with up to two sialic acid residues (done in
 CC recombinantly expressed G-CSF from CHO cells).
 CC -1- PHARMACOLOGICAL: Available under the names Neupogen or Granulokine
 CC (Amgen/Roche) and Granocyte (Rhône-Poulenc). Used to treat
 CC neutropenia (a disorder characterized by an extremely low number
 CC of neutrophils in blood).
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
 CC -1- CAUTION: Ref.4 misquotes the gene name as "CSF1".
 CC -1- DATABASE: NAME=Neupogen/Granulokine;
 CC NOTE=Clinical information on Neupogen/Granulokine;
 CC WWW=<http://www.neupogen.com/>.
 CC
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 CC
 CC EMBL; X03438; CAA27168.1; -
 CC EMBL; M13008; AAA03056.1; -
 CC EMBL; X03656; CAA27291.1; -
 CC EMBL; X03655; CAA27290.1; -

Query Match	Best Local Similarity	98.2%	Score 884.5	DB 1	Length 207
Matches 174	Conservative	0	Mismatches	0	Indels 3; Gaps 1
QY	2	TPLGASSLPDSGFLLKCLBQVRIQDGAALQKLVSECAATYKLCHEPSELVLLGSHGIP	58		
DB	31	TPLGASSLPDSGFLLKCLBQVRIQDGAALQKLVSECAATYKLCHEPSELVLLGSHGIP	90		
QY	59	WAPLSSCSQALQALGCLISQLSHGFLYXGGLQALGSLSPGLPTIDTQLDPAFATTI	118		
DB	91	WAPLSSCSQALQALGCLISQLSHGFLYXGGLQALGSLSPGLPTIDTQLDPAFATTI	150		
QY	119	WQWELGAPALPLOTQGAMPAPASAFORRAGGVVASHLQSFLEVSVYRLHLLAQ	175		
DB	151	WQWELGAPALPLOTQGAMPAPASAFORRAGGVVASHLQSFLEVSVYRLHLLAQ	207		

RESULT 3

CSF3_FELCA STANDARD; PRT; 194 AA.

AC 002708;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Granulocyte colony-stimulating factor precursor (G-CSF) (Fragment).

```

GN      Name=CSP3;
OC      Fells silvestris catus (Cat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
OC      Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felle.
OX      NCBI_TaxID=9685;
RN      (1)
RP      SEQUENCE FROM N.A.
RC      STRAIN=European shorthair; TISSUE=Lung;
RA      MEDLINE=21389237; PubMed=11497496; DOI=10.1006/cyto.2001.0910;
RX      Dunham S.P., Orlons D.E.;
RT      "Isolation, nucleotide sequence and expression of a cDNA encoding
RT      feline granulocyte colony-stimulating factor.";
RL      Cytokine 14:347-351(2001).
CC      -I- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC      cytokines that act in hematopoiesis by controlling the production,
CC      differentiation, and function of 2 related white cell populations
CC      of the blood, the granulocytes and the monocytes-macrophages. This
CC      CSF induces granulocytes (By similarity).
CC      -I- SUBUNIT: Monomer.
CC      -I- SUBCELLULAR LOCATION: Secreted.
CC      -I- PTM: O-glycosylated (By similarity).
CC      -I- SIMILARITY: Belongs to the IL-6 superfamily.
CC      -----
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CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC      or send an email to license@ebi.ac.uk).
CC      -----
DR      EMBL; Y08558; CAA69853.1; -.
DR      PIR; T09255; T09255.
DR      HSRF; P09919; IRHG.
DR      InterPro; IPR009079; 4 helix cytokine.
DR      InterPro; IPR003629; GCSF_MGF.
DR      InterPro; IPR003573; IL6_MGF_GCSF.
DR      InterPro; IPR003574; Interleukin_6.
DR      Pfam; PF00489; IL6; 1.
DR      PRINTS; PR00433; IL6GCSFMGF.
DR      PRINTS; PR00434; INTERLEUKIN6.
DR      ProDom; PD008386; GCSF_MGF; 1.
DR      SMART; SM00126; IL6; 1.
DR      PROSITE; PS00254; INTERLEUKIN_6; 1.
KM      Cytokine; Glycoprotein; Growth factor; Signal.
FT      NON TER 1
FT      SIGNAL <1 20 Potential.
FT      CHAIN 21 194 Granulocyte colony-stimulating factor.
FT      DISULFID 56 62 By similarity.
FT      DISULFID 84 94 By similarity.
FT      CARBOHYD 153 153 O-linked (GalNAc...) (By similarity).
SQ      SEQUENCE 194 AA; 21154 MW; P72B7AB3DAE7385E CRC64;

Query March 82.6%; Score 744; DB 1; Length 194;
Match Local Similarity 81.0%; Pred. No. 5,4e-60;
Matches 141; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

OY      2 TPLGPAASSLQSFLLKLCLEQVRKICGGGALQSRKCATYVLCHPEELVYLGHSLGIPWAP 61
DB      21 TPLGAPTSLSQSFLLKLCLEQVRKQVADGTLQSRKCAHGLCHPEELVYLGHSLGIPQAP 80
OY      62 LSSGSPQALQIACLSQLSHSGFLFYQGLQALLEGISPELGPTLDITQLDVADPATYIMQO 121
DB      81 LSSGSSQALQITGCLQRLHSGFLFYQGLQALAGISPELAPFTIDMQLDITDPAINIMQO 140
OY      122 MEELGAAPALQPTQGAAMPAPAFASFORRAGCVIVASHLQSFLEVSYRVLRLAOP 175
DB      141 MEDVGAPAPVPTQGTMPFTTSFAFORRAGGTVIVASNLQSFLEVAVYBALRHFTKP 194

RESULT 4
ID      Q9GJUU PRELIMINARY; PRT; 195 AA.
Q9GJUU

```

[illegible]

RT	"Cytsra structure of canine and bovine granulocyte-colony stimulating factor (G-CSF)." ;
RL	J. Mol. Biol. 224:640-653(1993).
CC	-1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are cytokines that act in hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages. This CSF induces granulocytes.
CC	-1- SUBUNIT: Monomer.
CC	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- PTM: O-glycosylated.
CC	-1- SIMILARITY: Belongs to the IL-6 superfamily.
DR	PDB; 1BGD; X-ray; @=1-175.
DR	PDB; 1BGE; X-ray; A/B=1-175.
DR	InterPro; IPR005079; 4_helix_cytokine.
DR	InterPro; IPR003629; GCSF_MGF.
DR	InterPro; IPR003573; IL6_MGF_GCSF.
DR	Pfam; PF00489; IL6; 1.
DR	PRINTS; PR00433; IL6GCSFMGF.
DR	PRODOM; PD008388; GCSF_MGF; 1.
DR	SMART; SMO0126; IL6; 1.
DR	PROSITE; PS00254; INTERLEUKIN_6; 1.
KW	3D-structure; Cytokine; Glycoprotein; Growth factor.
FT	DISULFID 37 43
FT	DISULFID 65 73
FT	CARBONYD 134 134
FT	STRAND 10 10
FT	HELIX 12 39
FT	HELIX 45 55
FT	TURN 56 56
FT	HELIX 63 65
FT	HELIX 67 69
FT	TURN 72 92
FT	HELIX 93 95
FT	TURN 98 100
FT	HELIX 101 125
FT	TURN 126 126
FT	HELIX 144 171
FT	TURN 172 172
FT	STRAND 173 173
SQ	SEQUENCE 175 AA; 18858 MM; 28C62A4990C6DB3 CRC64;
Query Match	82.0%; Score 739; DB 1; Length 175;
Best Local Similarity	80.6%; Pred. No. 1,de-55;
Matches 141; Conservative 11; Mismatches 23; Indels 0; Gaps 0;	
OY	1 MTPPLGPASSLPPOSFLKLCLEOVRCIOGDGAALOEKLCAATVKKCHEPELVLLGHSLGIPIWA 60
Db	1 MAPLGPGPDPSEFLKCLCEOMRKVDAGDLTOETLCATIQOLCHPEELVLIGHALGISIPOR 60
OY	61 PLSSCPESQALQLAGCLSQLHSGHFLTYOGLIQALEGISPELAPTLDTLQLDVADPATTIWQ 120
Db	61 PLSSCSSQALQINGCLRQHLSGFLVYGGLQDALAGISPFLAPLTDLTQLDPTDAINIMQ 120
OY	121 QMEELGNAPLLOPTQGAMPAPAFAPRRACGVLYASHLSFLEVSVRVLRHLAOP 175
Db	121 QMEDLGNAVPVPTQTGMTAPFAFSAFORRAGGVAVNSLOSFLBELAYALRHFPAP 175
RESULT 6	
CSF3_SHEEP	STANDARD; PRT; 174 AA.
ID	CSF3_SHEEP
AC	Q28746;
DT	30-MAY-2000 (Rel. 39, Created)
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DT	05-JUN-2004 (Rel. 44, Last annotation update)
DE	Granulocyte colony-stimulating factor (G-CSF).
GN	Name=CSF3;
OS	Ovis aries (sheep).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC	Caprinae; Ovis.
NCBI_TaxID=9940;	

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95102116; PubMed=7528579;
RA O'Brien P.M., Secow H.F., Rothen J.S., Wood P.R.;
RT "Cloning and sequencing of an ovine granulocyte colony-stimulating
RT factor cDNA."
RL DNA Seq. 4:339-342(1994).
CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC cytokines that act in hematopoiesis by controlling the production,
CC differentiation, and function of 2 related white cell populations
CC of the blood, the granulocytes and the monocytes-macrophages. This
CC CSF induces granulocytes (By similarity).
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: O-glycosylated (By similarity).
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC -----
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CC -----
DR EMBL, L07939; AAA68006.1; -.
DR PIR, T10268; T10268.
DR HSSP, P09919; 1RHG.
DR InterPro: IPR009079; 4 helix cytokine.
DR InterPro: IPR003629; GCSF_MGF.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR Pfam, PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR SMART; SM00126; IL6; 1.
DR Cytochrome; Glycoprotein; Growth factor.
FT DISULFID 36 42 By similarity.
FT CARBOHYD 133 133 O-linked (GalNAc...) (By similarity).
SQ SEQUENCE 174 AA; 18806 MW; BAA5A8F8D23ACDIE CRC64;

Query Match 81.9%; Score 738; DB 1; Length 174;
Best Local Similarity 82.2%; Pred. No. 1.7e-59;
Matches 143; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

QY 2 TPLGPASSLPQSFLLKCEQVRKIQGDAALOEKCATYKLCHEEVLVLSHSIGIPMAP 61
DB 1 TPLGPASSLPQSFLLKCEQVRKIQGDAALOEKCATYKLCHEEVLVLSHSIGIPMAP 60
QY 62 LSSCPSQALQLAGCLSQLHSGLFLYQGLQALLEGISPELGPTLDTLQDVADPATTIMQ 121
DB 61 LSSCPSQALQLAGCLSQLHSGLFLYQGLQALLEGISPELGPTLDTLQDVADPATTIMQ 120
QY 122 MELGMAAPALQPTQGMAPAFASAFORPAGVTVASHLQSFLEVSRYVLRHLAQP 175
DB 121 MELGMAAPALQPTQGMAPAFASAFORPAGVTVASHLQSFLEVSRYVLRHLAQP 174

RESULT 7
ID CSF3_BOVIN STANDARD; PRT; 195 AA.
AC P35833; Q9TV89;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Granulocyte colony-stimulating factor precursor (G-CSF).
GN Name=CSF3; Synonyms=GCSF;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos
NCBI_TaxID=9913;

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RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Holstein;
RA Heidari M., Kehrl M.E. Jr.;
RT "Cloning, sequencing and analysis of cDNA encoding bovine granulocyte
RT colony stimulating factor."
RL Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.
CC (2)
CC X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
CC MEDLINE=94076341; PubMed=7504736;
CC Lovejoy B., Cascio D., Eisenberg D.;
CC "Crystal structure of canine and bovine granulocyte-colony stimulating
CC factor (G-CSF)."
CC J. Mol. Biol. 234:640-653(1993).
CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC cytokines that act in hematopoiesis by controlling the production,
CC differentiation, and function of 2 related white cell populations
CC of the blood, the granulocytes and the monocytes-macrophages. This
CC CSF induces granulocytes.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: O-glycosylated.
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
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CC -----
DR EMBL, AF092533; AAD16102.1; -.
DR PDB; 1BGX; X-ray; @=22-195.
DR InterPro: IPR009079; 4 helix cytokine.
DR InterPro: IPR003629; GCSF_MGF.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR 3D-structure; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 195 Granulocyte colony-stimulating factor.
FT DISULFID 57 63
FT CARBOHYD 154 154 O-linked (GalNAc...) (By similarity).
FT CONFLICT 93 94 TS -> RG (in Ref. 2).
FT HELIX 32 60
FT HELIX 65 69
FT TURN 70 71
FT HELIX 72 75
FT TURN 76 76
FT HELIX 83 85
FT TURN 87 89
FT HELIX 92 112
FT TURN 113 115
FT TURN 118 120
FT HELIX 121 145
FT HELIX 164 191
FT TURN 192 192
SQ SEQUENCE 195 AA; 8066119E4ADF8A73 CRC64;

Query Match 80.7%; Score 727; DB 1; Length 195;
Best Local Similarity 81.0%; Pred. No. 1.9e-58;
Matches 141; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 2 TPLGPASSLPQSFLLKCEQVRKIQGDAALOEKCATYKLCHEEVLVLSHSIGIPMAP 61
DB 22 TPLGPASSLPQSFLLKCEQVRKIQGDAALOEKCATYKLCHEEVLVLSHSIGIPMAP 61
QY 62 LSSCPSQALQLAGCLSQLHSGLFLYQGLQALLEGISPELGPTLDTLQDVADPATTIMQ 121

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Db      82 LSSCSQSLQTLNSCLNQLHGGVFLVYQGLLQALAGISPELAPLDTLQDLVTDATNIMQ 141
Qy      122 MELGMAPLQPTQGMPPAFASFORRAGGVVASHLQSFLEVSRYVLRHIAOP 175
Db      142 MEDLGAAPVAPVPTQGMPTFTSAFORRAGGVVASHLQSFLEVSRYVLRHIAOP 195

RESULT 8
CSF3_PIG STANDARD; PRT; 195 AA.
ID CSF3_PIG 002837; 019180;
AC 002837; 019180; (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Granulocyte colony-stimulating factor precursor (G-CSF).
GN Name=CSF3;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_Taxid=9823;
RN (1)
RP SEQUENCE FROM N.A.
RA Kulmburg P.;
RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RA Tissue=Liver;
RC Sandeman R.M., Strom A.D.G.;
RA Glozier S.B.;
RT "Cloning of a cDNA and gene encoding porcine granulocyte-colony
RT stimulating factor."
RT Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC cytokines that act in hematopoiesis by controlling the production,
CC differentiation, and function of 2 related white cell populations
CC of the blood, the granulocytes and the monocytes-macrophages. This
CC CSF induces granulocytes (By similarity).
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: O-glycosylated (By similarity).
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
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CC -----
DR EMBL: Y10494; CAA71518.1; -
DR EMBL: U68482; AAB70701.1; -
DR EMBL: U68481; AAB70700.1; -
DR HSSP: P09919; 1RHG.
DR InterPro: IPR009079; 4_helix_cytokine.
DR InterPro: IPR003629; GCSF_MGF.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR SMART: PD008388; GCSF_MGF; 1.
DR PROSITE: PS00254; INTERLEUKIN_6_1.
DR Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 195 Granulocyte colony-stimulating factor.
FT DISULFID 57 63 By similarity.
FT DISULFID 85 95 By similarity.
FT CARBOHYD 154 154 O-linked (GalNAc...) (By similarity).
FT CONFLICT 123 123 A -> R (in Ref. 1).
FT SEQUENCE 195 AA; 21214 MW; 84787P20DBA8A1C CRC64;
SQ
Query Match 77.9%; Score 702; DB 1; Length 195;
Best Local Similarity 79.2%; Pred. No. 3.8e-56;

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Matches 137; Conservative 11; Mismatches 25; Indels 0; Gaps 0;
Qy      3 PLGPASSLPQSFILCLBQVRKIQGDGAALQCKLCATYKLCHEBELVLGHSIGIPMAPL 62
Db      23 PLSPASSLPQSFILCLBQVRKIQGDGAALQCKLCATYKLCHEBELVLGHSIGIPMAPL 82
Qy      63 SSCPSQALQTLNSCLNQLHGGVFLVYQGLLQALAGISPELAPLDTLQDLVADATNIMQ 122
Db      83 SSCPSQALQTLNSCLNQLHGGVFLVYQGLLQALAGISPELAPLDTLQDLVADATNIMQ 142
Qy      123 MELGMAPLQPTQGMPPAFASFORRAGGVVASHLQSFLEVSRYVLRHIAOP 175
Db      143 MEDLGAAPVAPVPTQGMPTFTSAFORRAGGVVASHLQSFLEVSRYVLRHIAOP 195

RESULT 9
CSF3_MOUSE STANDARD; PRT; 208 AA.
ID CSF3_MOUSE P09920;
AC P09920;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Granulocyte colony-stimulating factor precursor (G-CSF).
GN Name=CSf3; Synonyms=Csfg;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
RN (1)
RP SEQUENCE FROM N.A.
RA MEDLINE=87017003; PubMed=3489940;
RA Tsuchiya M., Asano S., Kaziro Y., Nagata S.;
RT "Isolation and characterization of the cDNA for murine granulocyte
RT colony-stimulating factor."
RT Proc. Natl. Acad. Sci. U.S.A. 83:7633-7637(1986).
RN (2)
RP SEQUENCE FROM N.A.
RA MEDLINE=87190474; PubMed=3494605;
RA Tsuchiya M., Kaziro Y., Nagata S.;
RT "The chromosomal gene structure for murine granulocyte colony-
RT stimulating factor."
RT Eur. J. Biochem. 165:7-12(1987).
RN (3)
RP PARTIAL SEQUENCE.
RX PubMed=3501294;
RA Simpson R.J., Nice E.C., Nicola N.A.;
RT "Structural studies on the murine granulocyte colony-stimulating
RT factor."
RT Biol. Chem. Hoppe-Seyler 368:1327-1331(1987).
CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC cytokines that act in hematopoiesis by controlling the production,
CC differentiation, and function of 2 related white cell populations
CC of the blood, the granulocytes and the monocytes-macrophages. This
CC CSF induces granulocytes.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: O-glycosylated (By similarity).
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M13926; AAA37672.1; -
DR EMBL: X05402; CAA28986.1; -
DR PIR: A29536; A26496.
DR HSSP: P09919; 1RHG.
DR InterPro: IPR009079; 4_helix_cytokine.

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DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Direct protein sequencing; Glycoprotein; Growth factor;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 208 Granulocyte colony-stimulating factor.
FT DISULFID 72 78 By similarity.
FT DISULFID 100 110 By similarity.
FT CARBOHYD 169 169 O-linked (GalNAc...) (By similarity).
SQ SEQUENCE 208 AA; 22421 MW; 0BF3622135C906DB CRC64;

Query Match 71.3%; Score 642; DB 1; Length 208;
Best Local Similarity 74.6%; Pred. No. 1.2e-50;
Matches 129; Conservative 11; Mismatches 33; Indels 0; Gaps 0;

Qy 1 MTPLGPAASSLPQSFLLKLEQVRKIQGDGAALQEKLCATYKLCHEBELVLLGHSIGIPWA 60
Db 36 VSALPPSLPLPRSFLLKLEQVRKIQAGSSVLLBQLCATYKLCHEBELVLLGHSIGIPWA 95
Qy 61 PLSSCPSQALQAGLSQHSGLFLYQGLQALAGISPELPTLDTLQDVADFATTIWO 120
Db 96 SLSSCSSQALQOTKLSQHSGLFLYQGLQALAGISPELPTLDTLQDVADFATTIWO 155
Qy 121 QMEELGMAPALOPTOGAMPAPAFASAFORRAGVTVASHLOSFLVSVRYLRHIA 173
Db 156 QMENIGVAPVPTOPTOSAMPAPAFASAFORRAGVTVASHLOSFLVSVRYLRHIA 208

RESULT 10
P97712 PRELIMINARY; PRT; 214 AA.
AC P97712;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Granulocyte colony stimulating factor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97074656; PubMed=8917083; DOI=10.1016/0378-1119(96)00131-X;
RA Han S.W., Ramesh N., Osborne W.R.;
RT "Cloning and expression of the cDNA encoding rat granulocyte colony-
RT stimulating factor";
RL Gene 175:101-104(1996).
DB EMBL; U37101; AAC52915.1; -.
DB PIR; JCS043; JCS043.
DB HSSP; P09919; 1R8G.
DR GO; GO:0005576; C:cytokine activity; IEA.
DR GO; GO:0005125; F:growth factor activity; IEA.
DR GO; GO:0008083; F:immune response; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 214 AA; 23659 MW; 29BB88B17B64C55 CRC64;

Query Match 70.5%; Score 635; DB 2; Length 214;
Best Local Similarity 72.6%; Pred. No. 5.6e-50;
Matches 127; Conservative 12; Mismatches 36; Indels 0; Gaps 0;

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Qy 1 MTPLGPAASSLPQSFLLKLEQVRKIQGDGAALQEKLCATYKLCHEBELVLLGHSIGIPWA 60
Db 27 VSSLPPSLPLPRSFLLKLEQVRKIQARNTTELLBQLCATYKLCHEBELVLLGHSIGIPWA 86
Qy 61 PLSSCPSQALQAGLSQHSGLFLYQGLQALAGISPELPTLDTLQDVADFATTIWO 120
Db 87 SLSSCSSQALQOTKLSQHSGLFLYQGLQALAGISPELPTLDTLQDVADFATTIWO 146
Qy 121 QMEELGMAPALOPTOGAMPAPAFASAFORRAGVTVASHLOSFLVSVRYLRHIA 175
Db 147 QMENIGVAPVPTOPTOSAMPAPAFASAFORRAGVTVASHLOSFLVSVRYLRHIA 201

RESULT 11
Q8MKE0 PRELIMINARY; PRT; 127 AA.
ID Q8MKE0;
AC Q8MKE0;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Granulocyte colony-stimulating factor.
CN Name=G-CSF;
OC Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Noronha L.E., Takafuji V.A., Sharova L.V., Crisman M.V., Howard R.D.;
RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF503365; AAM34205.1; -.
DR HSSP; P35833; 1BGC.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 127 AA; 13657 MW; 25559C2569802077 CRC64;

Query Match 56.7%; Score 511; DB 2; Length 127;
Best Local Similarity 79.5%; Pred. No. 7e-39;
Matches 101; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

Qy 49 VILGHSIGIPWAPLSSCPSQALQAGLSQHSGLFLYQGLQALAGISPELPTLDTLQ 108
Db 1 MLGHSIGIPWAPLSSCPSQALQAGLSQHSGLFLYQGLQALAGISPELPTLDTLQ 60
Qy 109 LDVADFATTIWOQMEELGMAPALOPTOGAMPAPAFASAFORRAGVTVASHLOSFLVSVRY 168
Db 61 LDVADFATTIWOQMEELGMAPALOPTOGAMPAPAFASAFORRAGVTVASHLOSFLVSVRY 120
Qy 169 LRHIA 175
Db 121 LRHIA 127

RESULT 12
MGF_CHICK STANDARD; PRT; 201 AA.
ID MGF_CHICK;
AC P13854;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Myelomonocytic growth factor precursor (MGF).
OS Gallus gallus (Chicken).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89231616; Pubmed=2785450;
 RA Leutz A., Damm K., Sterneck B., Kowenz B., Nees S., Frank R.,
 RA Gausepohl H., Pan Y.-C.E., Smart J., Hayman M., Graf T.;
 RT "Molecular cloning of the chicken myelomonocytic growth factor (CMGF)
 RT reveals relationship to interleukin 6 and granulocyte colony
 RT stimulating factor.";
 RL EMBO J. 8:175-181(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92195319; Pubmed=1549124;
 RA Sterneck E., Blattner C., Graf T., Leutz A.;
 RT "Structure of the chicken myelomonocytic growth factor gene and
 RT specific activation of its promoter in avian myelomonocytic cells by
 RT protein kinases.";
 RL Mol. Cell. Biol. 12:1728-1735(1992).
 CC -1- FUNCTION: Hematopoietic growth factor that stimulates the
 CC proliferation and colony formation of normal and transformed avian
 CC cells of the myeloid lineage.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
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DR EMBL; M85034; AAA48694.1; -;
 DR EMBL; X14477; CAA32639.1; -;
 DR PIR; A42247; A42247.
 DR HSSP; P09919; 1RHG.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR003629; GCSF_MGF.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PRO0433; IL6GCSFMGF.
 DR PRINTS; PRO0434; INTERLEUKIN_6.
 DR ProDom; PD008388; GCSF_MGF; 1.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR GlycoSite; Growth factor; Signal.
 FT CHAIN 1 23
 FT DISULFID 24 201
 FT DISULFID 61 67
 FT DISULFID 89 99
 FT CARBOHYD 123 123
 FT CARBOHYD 137 137
 SQ SEQUENCE 201 AA; 22373 MW; 2408DD21B424466 CRC64;

Query Match 33.7%; Score 304; DB 1; Length 201;
 Best Local Similarity 40.6%; Pred. No. 1e-19;
 Matches 67; Conservative 28; Mismatches 68; Indels 2; Gaps 1;

QY 12 QSTFLKLEGVKRIQDGAALQKCATYKLCHEPEVLVILGSLGIRMAVLLSCPSQALQ 71
 DB 36 QFLHNKLETRKIRGVALORAVCDTFOCTEEELQVOPPHVQALDQCHKRGFQ 95
 QY 72 LAGCLSHSGGLFYQGLQALGSLSPGLPTLDTLOLDVADPATTTWQMEELGNAPAL 131
 DB 96 AEVCFQIRAGLAVYHDSLCAVRLRLPNHTTVETLDDAANLSSNIGQOMEDLGLDPTV 155
 QY 132 QPTQ--GAMPAPASAFQRRAGVTVASHLQSFLEVSRYVLRHLAQ 174

DB 156 LPBAQSPPTPTSGPFOQGVGFILANFQRLTAAYRALRLHAR 200
 RESULT 13
 ID Q90Y10 PRELIMINARY; PRT; 241 AA.
 AC Q90Y10;
 DT 01-DEC-2001 (TEMBLrel. 19, Created)
 DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE Interleukin-6 precursor.
 GN Name=IL-6;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schneider K., Klaas R., Kaspers B., Staeheli P.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kaiser P., Rothwell L., Gallov E.E., Barrow P.A., Burnside J.,
 RA Mingley P.;
 RT "Differential cytokine expression in avian cells in response to
 RT invasion by Salmonella typhimurium, Salmonella enteritidis and
 RT Salmonella gallinarum.";
 RL Microbiology 146:3217-3226(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kaiser P.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ309540; CAC40812.1; -;
 DR EMBL; AJ250838; CAC15566.2; -;
 DR HSSP; P05231; IALD.
 DR GO; GO:000576; C:extracellular; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PRO0433; IL6GCSFMGF.
 DR PRINTS; PRO0434; INTERLEUKIN_6.
 DR ProDom; PD008388; GCSF_MGF; 1.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR GlycoSite; mature ChIL-6.
 FT CHAIN 1 47
 FT DISULFID 48 241
 SQ SEQUENCE 241 AA; 26790 MW; 657F8049F25BD2F8 CRC64;

Query Match 12.3%; Score 111; DB 2; Length 241;
 Best Local Similarity 22.2%; Pred. No. 0.055;
 Matches 46; Conservative 35; Mismatches 74; Indels 52; Gaps 7;

QY 4 LBPASLTP-----QSFLKLEGVKRIQDGAALQKCATYKLCG 44
 DB 41 LPPAAVPLPAAADSGEVGLBEAGARALDCEPLAVLDRAVQLODBMCKRTVCE 100
 QY 45 PEELVLLGSLGIPWAPLSSCPQALQLAG-----CLQSHSGGLFYQGLQALGSLSP 99
 DB 101 NSWEMLVRRNNLPL-----KVTEEDGILAGFBEKLTTLSSGLFAFYLERIGETPDS 156
 QY 100 LQPTLDTLOLDVADPATTTWQMEELGNAPALOPTQGAMPAPASAFQRRAGVTV----- 153
 DB 157 EKQWVESLCYSTRKLAATIRQV-----INPDEVIP--DSAQKSLANLKSXDKW 206
 QY 154 ---VASHL-----QSFLVSRYVLRHL 172
 DB 207 IKTIMHLIRDFTSMEKTVRAVRYL 233

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RESULT 14
Q8MJ75 PRELIMINARY; PRT; 212 AA.
ID Q8MJ75
AC Q8MJ75;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE IL-6.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee D., Yoo H., Choi I.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF518322; AMN74938.1; -.
DR HSBP; P05231; IALU.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:Cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix_cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 212 AA; 23881 MW; 1F540E7030BCFD77 CRC64;

Query Match
Best Local Similarity 23.3%; Score 110.5; DB 2; Length 212;
Matches 37; Conservative 32; Mismatches 85; Indels 5; Gaps 3;

QY 17 KCLEGVRIQGDGAALQEKLCATYKLCHEPELVLLGHSLGIP-WAPLSSCPSQLQIAGC 75
DB 52 KTEBELIKYILGKISAMREKCEKYCKCENSKVLAENNLNLPKMAEKDGCFOGSGFNGETC 111
QY 76 LSQHSGLFLYQGLQALBGISPELPTLDTLQLDVADFAFTTWQMEELGMAPALOPT- 134
DB 112 LMRITTVLVEFOIYLDYLOKYEYSNKNQNEAVQISTKALIQTLROKGNKPKDKATTNPPT 171
QY 135 -QGAPAFAS--AFQRRAGGVLAASHQSFLEYSYVLR 170
DB 172 NAGLDDKLOSQNEWMKNTKIILRLSEDFLOPSLRAIR 210

RESULT 15
Q9XT80 PRELIMINARY; PRT; 208 AA.
ID Q9XT80
AC Q9XT80;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Interleukin 6.
OS Delphinapterus leucas (beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Monodontidae; Delphinapterus.
OC NCBI_TaxID=9749;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20141864; PubMed=10678396; DOI=10.1016/S0165-2427(99)00150-6;
RA St-Laurent G., Archambault D.;
RT "Molecular cloning, phylogenetic analysis and expression of beluga
whale (Delphinapterus leucas) interleukin 6."
RL Vet. Immunol. Immunopathol. 73:31-44(2000).
DR EMBL; AF076643; AAD42929.1; -.
DR HSBP; P05231; IALU.
DR GO; GO:0005576; C:extracellular; IEA.
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DR GO; GO:0005125; F:Cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix_cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 208 AA; 23456 MW; 81CC85C6E80389C4 CRC64;

Query Match
Best Local Similarity 21.3%; Score 108; DB 2; Length 208;
Matches 33; Conservative 35; Mismatches 81; Indels 6; Gaps 2;

QY 22 VKRIQGDGAALQEKLCATYKLCHEPELVLLGHSLGIP-WAPLSSCPSQLQIAGC 80
DB 52 IKYILGKISAMREKCEKYCKCENSKVLAENNLNLPKMAEKDGCFOGSGFNGETC 111
QY 81 SGLFLYQGLQALBGISPELPTLDTLQLDVADFAFTTWQMEELGMAPALOPTOGA--- 137
DB 112 TGLLEVOIYLDYLOKYEYSNKNQNEAVQISTKALIQTLROKGNKPKDKATTNPPT 171
QY 138 -MPAFASAFQRRAGGVLAASHQSFLEYSYVLR 170
DB 172 NNLQSDNDWMKNTKIILRLSEDFLOPSLRAIR 206
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Search completed: July 9, 2005, 12:53:58
Job time : 111.819 secs